FIG. 1

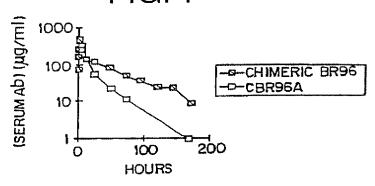


FIG. 2

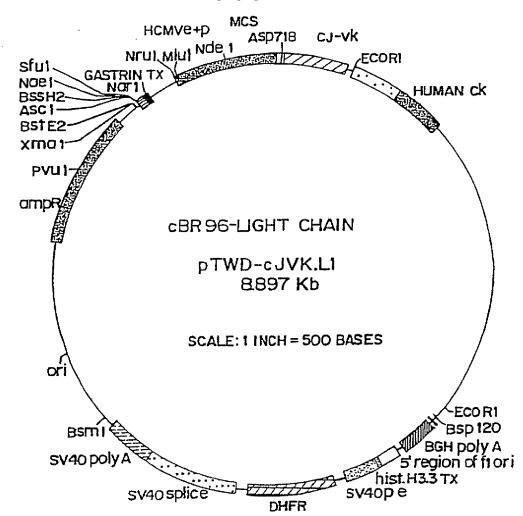


FIG. 3 sfu1 Gastrin TX BSSH2 Nru1

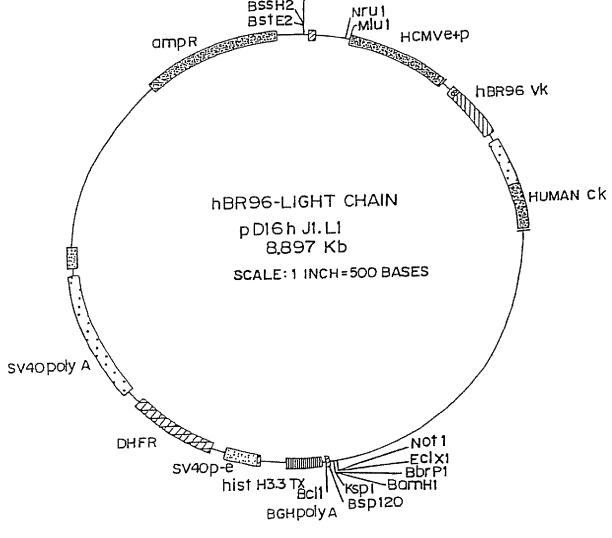


FIG. 4

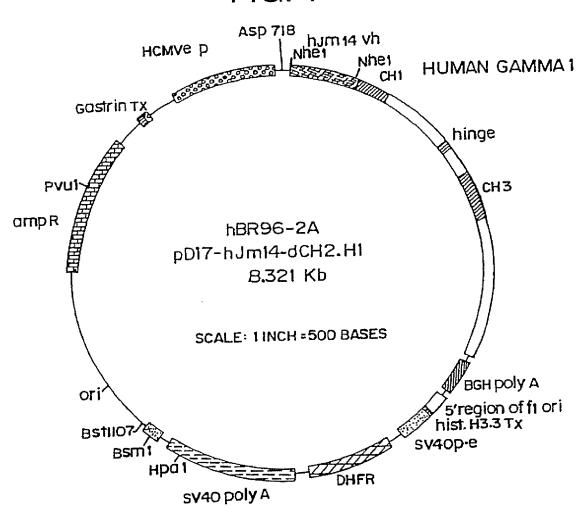


FIG. 5

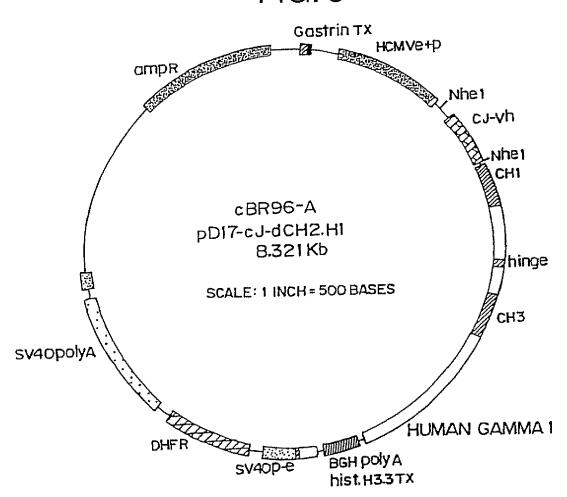


FIG. 6

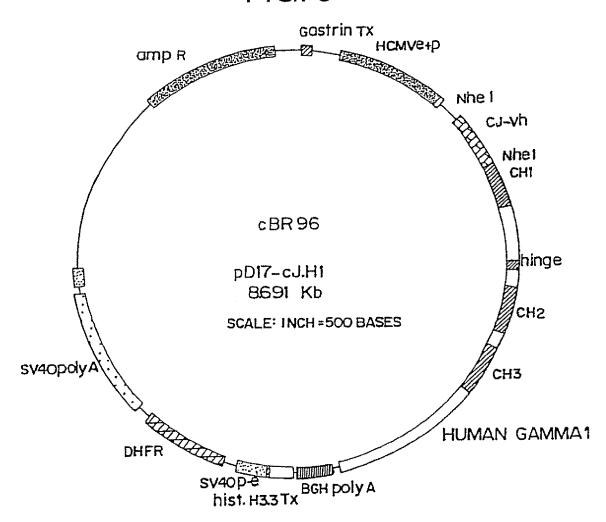


FIG. 7

hBR96-2A DOX

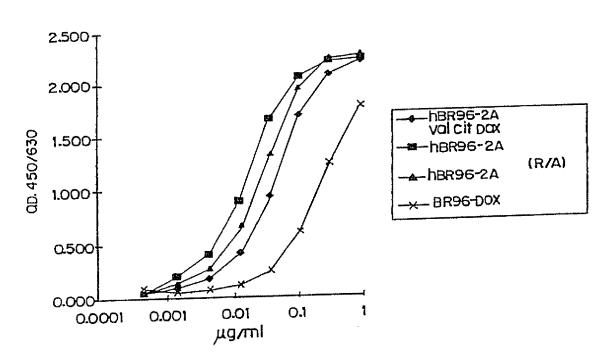


FIG. 8

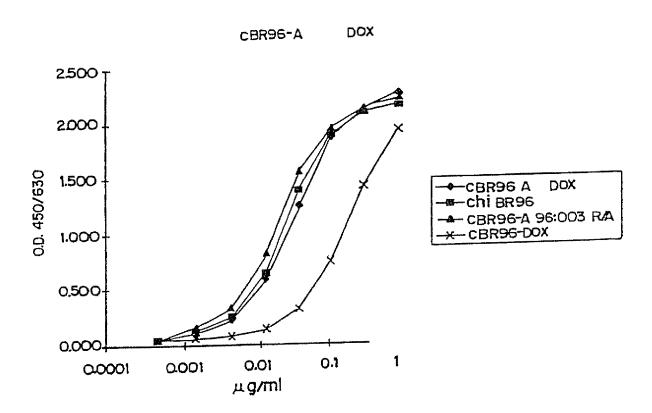


FIG. 9A

A-HINGE + CH2 + CH3 DOMAINS WERE REMOVED FROM BR96 IGGI CONSTRUCT BY E.CO.47-III RESTRICTION DIGESTION.

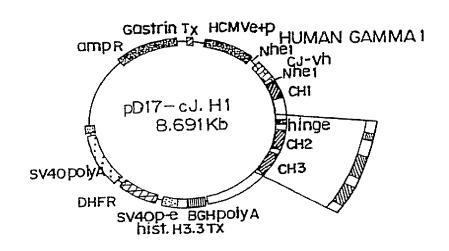


FIG. 9B

B-HINGE+CH3 DOMAINS AMPLIFIED BY PCR FROM L6 IGG1 CONSTRUCT LACKING THE CH2 DOMAIN.

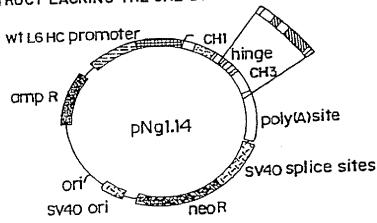
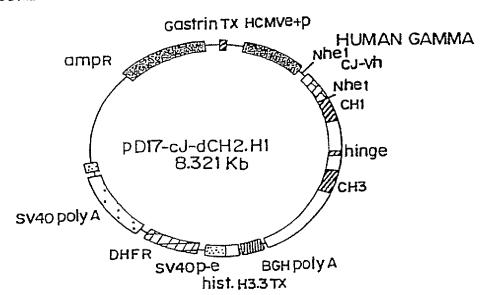


FIG. 9C

C.-HINGE+CH3 PCR FRAGMENT CLONED BY HOMOLOGOUS RECOMBINATION INTO E.CO.47-III SITE OF BR96 IGGI MOLECULE.



1.- INTRODUCTION OF MUTATIONS BY SITE DIRECTED MUTAGENESIS ON DOUBLE-STRANDED PLASMID DNA.

FIG. 10A

A.- MUTATIONS INTRODUCED INTO SYNTHETIC OLIGONUCLEOTIDES USED FOR THE PCR AMPLIFICATION OF CH2 DOMAIN

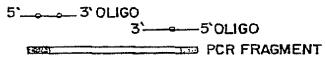


FIG. 10B

B.-PLASMID DNA LINEARIZED INSIDE CH2 DOMAIN AND COTRANSFORMED WITH PCR FRAGMENT INTO COMPETENT DH5a



FIG. 10C

C. CLONING MEDIATED BY HOMOLOGOUS RECOMBINATION YIELDS TRANSFORMANTS HARBOURING RECOMBINANT PLASMIDS.



FIG. 11

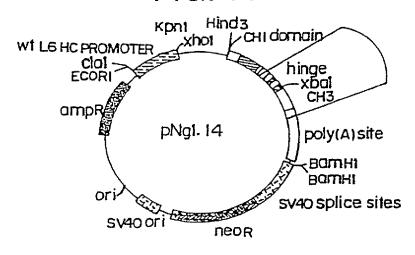


FIG. 12

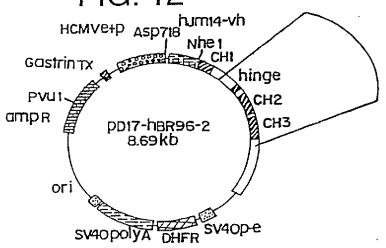


FIG. 13

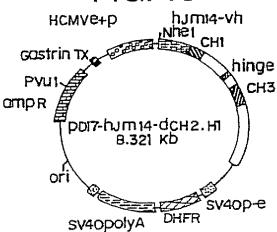


FIG. 14A
Primary Sequence = SEQ ID NO:10
Complementary Sequence = SEQ ID NO:28

CGGTGGGAGG GCCACCCTCC AAATGGCCCG TTTACCGGGC TACCACTACG CCCTCAAACA GGGAGTTTGT 540 GGCTGACCGC CCGACTGGCG TGGGTGGACT ACCCACCTGA 450 270 AATTGCATGA AGTTATTAAT GAACTGGCTG TTAACGTACT TCAATAATTA AGCCAGTATC TCGGTCATAG AATAAAATAA TAGGCGTGTA ATCCGCACAT ACTGCAGTTA CAATGACGGT GCGATAATGG 800 TGACGICAAT CGCTATTACC GITTACTGCCA ATTATTGACT CAACTGIAAC TAATAACTGA TGGCCCGCCT ACCGGGCGGA TIGACGICAA AACTGCAGTT CTTGACCGAC CGCATAGTTA GCGTATCAAT ATTABARTAR TAATTTATT 170 ANATGGGCGG TTTACCCGCC ATGTAGATGC ATAATCAGTA TCCACCCAT AGGTGGGGTA 790 AATGCCATTT CTATTGACGT GATAACTGCA TATTAGTCAT GGACTTTCCA CCTGAAAGGT 610 TTACGGTAAA GITCCGITCC 340 GITGACATIG Chaggchagg GGAAAAAAA GCTCTGATGC CGAGACTACG 250 CCTTTTTTT 160 GGTAACTGCG TITCCAAGIC AAAGGITTCAG CCATTGACGC 870 TACATCTACG AGTACGCCCC TCATGCGGGG GTTACATAAC CAATGTATTG ACCCCAATAG TGCGGTTATC 150 AGTACAATCT AGATATACGC TCTATATGCG ATTCGATGTT 240 TAAGCTACAA CGGTCTCATT TCATGTTAGA GCCAGAGTAA GTTGAGGCGG CHACTCCGCC 500 TCCCATAGEA CCCTGAAAGG ATGAACCGTC GAGTGCCCT CTCACGGGGA TACTIGGCAG 860 TCATATGCCA TAGITICACAT AGTATACGGT 680 AGGGTATCAT ACATGCCCGG GGAGITCCGC CCTCAAGGCG TGTACGGGCC GICGACTOTO GAGCAAAATT CTCGTTTAA CAGCTGAGAG 230 CGAAGCTTAT GCTTCGAATA 140 AATGTCGTAA TTACAGCATT AGCGGTTTGA TCGCCAAACT GGGACTITCC ATCAAGTGTA 670 TGACGTATGT ACTGCATACA GCCCATATAT CGGGTATATA 490 ACGAAGCGCT TCATCACGCG 310 TGCTTCGCGA 400 TAGGGGATAC AGTAGTGCGC ATCCCCTATG TCCGCGCGC AGGCGCGCCG 130 220 GACTTTCCAA CIGARAGGIT GGGCGTGGAT CCCGCACCTA 840 ATGACCTTAT TACTGGAATA AACCGTCATG TIGGCAGIAC ACCTCAATAA 660 CGTTTTGCGC GCAAAACGCG AATCAAGTAT 480 TGCAGTTATT 570 TTAGTTCATA 390 CTCCAGCGAC CGATCTCCCG GCTAGAGGGC GAGGTCGCTG 210 AGGTGACCTG TCCACTGGAC AAACCGTGGT TTTAGTTGCC AAATCAACGG GTACATCAAT CATGINGITA TGCCCAGIAC AACTGCCCAC TTGACGGGTG ACGGGTCATG CCGCCCATTG 650 GGCGGGTAAC 560 TCATTAGTTA ATGCCCCAGT TAGGGTTAGG TCTTAGACGA ATCCCAATCC TACGGGGGTCA TIGIGIGITG AACACACAAC AGTTTGGCGC CTCTAGACGA TCAAACCGCG 200 110 GAGATCTGCT TTTGGCACCA CCTGGCATTA GGTTTTGGCA CCANANCCGT ATTTACGGTA GGACCGTAAT CCAACGACCC TAAATGCCAT GGTTGCTGGG AGTAATCAAT AGAATCTGCT ACGAGGGACG AAACTCTACC TGCTCCCTGC TTTGAGATGG GACGGATCGG CTGCCTAGCC

TGGGTCTGGA

GTCGAACCCG

ACGGGGAGGTC

13/53

FIG. 14B Primary Sequence = SEQ ID NO:10

Complementary Sequence = SEQ ID NO:28 GTTGGTGAGA Chaccacter CACCAGIGGC 1530 TGCCACAGCA GIGGICACCG GTCTTCCCCC CAGAAGGGGG GCAAGAGGCC 1440 CGTTCTCCGG CGATTCACCA 1350 TAGGICIGIG ACAITICCCA GCIAAGIGGI 1170 CAAGCGGTCT TCTGGGGGAG CACTICACIT AGACCACCIC AGACCCCCIC GITCGCCAGA GAGACCCAAG CGAACGATCG CTCTGGGTTC CCTGTTCTTT CGAACCGGTG GCTTGGCCAC CCTCAGCAGC GGAGTCGTCG GGACAAGAAA GGGCCCATCG CCCGGGTAGC 1610 GTATTACTGT CATAATGACA 1520 GTACATAACC TGTAAAGGGT 1430 CATGTATTGG TCTGGTGGAG 1340 1160 TCTTGCGGCC AGAACGCCGG AGTGATATCC TCACTATAGG ACACCAAGGT TGTGGTTCCA ACTACTTCCC TGATGAAGGG GACTCTACTC CTGAGATGAG CTAGCACCAA 1600 GTGACTATTA ACACAGCCAT 1510 GATCGTGGTT TGTGTCGGTA ATCCAGACAC GTGAAGTGAA GCTAACCTTA 1150 1240 AATTATGCTG CGATTGGAAT TTAATACGAC 1060 AAGCCCAGCA Treggereer CTGGTCAAGG CAGTCCTCAG GTCAGGAGTC GACCAGITCC 1770 TTCAGACTCC GTCTCTGTAG TATTGGCTGA AAGTCTGAGG 1500 CAGAGACATC ATAACCGACT TTCACTTTCA 1320 GGTGTCCAGT CCACAGGTCA 1230 AAGTGAAAGT 1410 TGGCCAGTTA ACCEGICAAT CTTATCGAAA GAATAGCTTT 1050 CGTGAATCAC GCACTTAGTG CCTGGGCTGC GGCTGTCCTA CCGACAGGAT 1670 GAGCCGTCTG TCTGGTCACG AGACCAGTGC GGACCCGACG CTCGGCAGAC 1490 AGGTGGTGAT TTGGAGACCT TCCACCACTA 1400 AACCTCTGGA 1310 1220 TCTCTAGATA AGAGATCTAT TGTTTTAAA ACANAATTTT ACGNATGACC TGCTTACTGG 1130 ACATCTGCAA TGTAGACGTT ACACCITCCC GCCAAGGGAC GCACAGCGGC TGTGGAAGGG CGGTTCCCTG CGTGTCGCCG 1660 1570 ACCTGCAAAT TGGACGTTTA 1480 TGTAATCAGT CGAACCAGGA AGGAACAGGA AGGGACTTTC AGAGGACACA ACATTAGTCA 1390 TCTCCTGTGT 1210 1300 AGGTCTCGAG TCCTTGTCCT TCCAGAGCTC GAGAACCCAC CTCTTGGGTG 1120 ACCCAGACCT AGCGGCGTGC TCGCCGCACG ACCTCTGGGG TEGAGACCCC 1650 CGAATGACCC TTGTGGGACA GCTTACTGGG CICCGACCIC ACCCAGCGIA AACACCCTGT TGGGTCGCAT TCCCTGAAAG 1290 1380 1470 GCTTGGTCCT ATATCTCCTT TATAGAGGAA TGGCTAACTA ACCGATTGAT 1110 1020 CAGCTTGGGC CGCCCTGACC GCGGGACTGG CTCCAAGAGC GAGGTTCTCG 1640 GAGGCTGGAG CAATGCCAAG GTTACGGTTC GGCCTGGTTT CCGGACCAAA CGGACCTCCC 1460 GCCTGGAGGG 1280 AACACCAATT GTCTCGAGAG ATTTAAATTG TAAATTTAAC TTGTGGTTAA CAGAGCTCTC 1190 1010 TGCCCTCCAG GGAACTCAGG CCTTGAGTCC TGGCACCCTC ACCOTGGGAG ACCTGCTGCC TGGACGACGG TCTCCAGAGA AGAGGTCTCT CTCCAGAGAA GAGGTCTCTT GCTTAGTGCA CGAATCACGT CACCATGGAG GTGGTACCTC 1180 CTTGGTACCA GAACCATGGT TCTATATAG AGATATATTC

FIG. 14C

Primary Sequence = SEQ ID NO:10 Complementary Sequence = SEQ ID NO:28

ACACGCAGAA TGTGCGTCTT 2430 ACATCGCCGT TCTACAGCAA GTGTCCACAT AGATGTCGTT CACAGGTGTA TGTAGCGGCA CCAGGCCTCG 2340 GCCACATGGA COGTGTACCT 2160 GGICCGGAGC GGTCTAAGGT TTTCCCCAG ANANGGGGTC GAGCCATATC CTCGGTATAG CCAGATICCA TCAGGTCCCG CACAACCACT GGCACTACGT ACTCCGAGAC GTGTTGGTGA TATCCCAGCG GITICCGAAG ATAGGGICGC TCCTTCCT GAGGCTGCCG AGGAAGAAGG CCCCGAGAAC CATTCGGTCG CATGTCCGGA GGGGCTCTTG AAGAGAGGAG GTAAGCCAGC GTACAGGCCT TTCTCTCTC 2330 2420 GACCTGCCAA ATGCAGCCCC TCTTCTGGCT AGAAGACCGA CTGGACGGTT 2150 TACGTCGGGG TGAGGCTCTG CAAAGGCTTC CTCCGACGG TACAGGGCAG ATGICCCGIC 2680 CCGTGCCCAG TGGGTACCAA GGCACGGGTC 2320 ACCCATGGTT 2140 GAGCCTGTGG CTCGGACACC 2410 AGGGAGAGGG TCCCTCTCCC GCTGGGCTCA CGACCCGAGT CATCCCGGCT GTAGGGCCGA 1960 1870 CCGTGATGCA GGACGGACCA GGAGACAGGG CCGTGCTGGA GGCACGACCT 2670 CCTCTGTCCC TGTGTGCTGC CCTGCCTGGT ACACACCACG 2400 TGAGGGAGTC CACATGCCCA GTGTACGGGT ACTCCCTCAG ACTCATGCTC TGAGTACGAG AGGGGCAGGT TCCCCGTCCA 2130 2310 TGCCTGGACG AGTCGCGAGG ACGGACCTGC 1950 2040 CCCCTTGCAG AAGAGTACGA TTCTCATGCT TGGTGCGGAG 2660 ACCACGCCTC 2480 GTCAGCCTGA CAGTCGGACT GCATCCAGGG CGTAGGTCCC 2390 GCTGTACCAA CGACATGGTT TGTTTTGAGT ACAAAACTCA 2300 ACGGGCGGGG CTGCACACAA CAAACTCTCC GTTTGAGAGG TGCCCGCCCC 2030 GACGTGTGTT TCAGCGCTCC 1940 GGGGAACGTC CAACTACAAG 2650 GTTGATGTTC CAAGAACCAG GTTCTTGGTC TCTCATCGGA GAGAGTGACC CTCTCACTGG AGAGTAGCCT 2380 AAATCTTGTG TTTAGAACAC 2290 2470 CCCCAAAGGC AACCCAGGCC TTGGGTCCGG 2110 GGGGTTTCCG CGGAGGCCTC 2200 GAAGCCAGGC 1930 GCCTCCGGAG 2020 CTTCGGTCCG CCACCGTCGT GGTGGCAGCA TACTCGACTG AGCCGGAGAA TCGGCCTCTT ATGAGCTGAC CAGGTGCCCT GGAGACGGGA GTCCACGGGA 2370 CCTCTGCCCT TGCAGAGCCC ACGTCTCGGG 2280 2460 TCCACGGGGA CCTAAGCCCA GGATTCGGGT 2190 AGGTGCCCCT 2100 GTGTCTGCTG CCTCTTCACC 2010 CACAGACGAC 1920 GGAGAAGTGG CTGTTCTCGT GACAAGAGCA GGTAGGGCCC AGCAATGGGC TCGTTACCCG 2630 CCATCCCGGG CTCGGCCCAC GAGCCGGGTG CAAGGCGGGA 2450 2540 TAGAAGAGAG GTTCCGCCCT CTGCCCCTGA 2180 ATCTTCTCC 2270 GCCCCGTCTG GGCACAGGCT CCGTGTCCGA 2090 GACGGGGACT CGGGGCAGAC GGGAGGGAGG CCCTCCCTCC 1910 GCTCACCGTG CGAGTGGCAC GGAGTGGGAG CCTCACCCTC CACCCTGCCC GTGGGACGGG CCCTCCAGCT CAGAGGCCGG GTCTCCGGCC GTAACTCCCA CATTGAGGGT GGGAGGTCGA CGGGAGGACC GCCCTCCTGG AGCAAGGCAG TCGTTCCGTC GCTCTGGGCA CGAGACCCGT GCCAGCACA CCGGTCGTGT

FIG. 14D

Primary Sequence = SEQ ID NO:10

= **SEQ ID NO:28** Complementary Sequence TCAGACAAAC AGTCTGTTTG 3150 3240 3330 CCTGTGGAGG GGACACCTCC CACCACACAC Greererere GAACACTCCT CTTGTGAGGA CTACCCCCAC 3060 GATGGGGGTG TTCTGTGAGC CTGACAGGAC AAGACACTCG 2970 TGTGCAGGTG ACACGICCAC AGCAGCACCT TCGTCGTGGA TACCAAGAAA TGCTTGGCAC ATGGTTCTTT ACGAACCGTG GCTGACCTGC CGACTGGACG GCCACACGGC TCGCACACGT CCTCACCCAT GGAGTGGGTA ACTCTCGGGC AGCGTGTGCA GACTGTCCTG 3230 3320 CCCTGTACG TGAGAGCCCG 3410 CGGTGTGCCG CCCTCCCTCC GGGAGGGAGG 3140 ACCEGGGTCCG CGAGACTGTG GCTCTGACAC TGGCCCAGGC 3050 CGCACGAGGA dcgractccr 2960 TICICCACAT AAGAGGTGTA GGGGACATGC 3400 AGGTTGGCCG 3490 AGCAAGGICC TCGTTCCAGG ACAGGCCCTC TCCAACCGGC TGTCCGGGAG CTCTGTAGGA GAGACATCCT 3220 CAGGGGTGTG GCCAGCGTGG CGGTCGCACC 3310 GTCCCCACAC 3040 ACCCGGGGGAC 3130 2860 TGGGCCCCTG CTCTCGCGGT GAGAGCGCCA 2950 CCCCGCACTG CCCAGACCAG TCTCGGCAGC AGAGCCGTCG 3480 GGGTCTGGTC 3570 AACCGACTCC GGGGCGTGAC TTGGCTGAGG ACCCCCTAAA CAGCCCCTGC 3210 GTGCGTAGGG CACGCATCCC 3300 3390 TGGGGGATTT GTCGGGGACG 3030 CCCAGGGTGA CGAGGGGCCC AGCGCTGCCC TCGCGACGG 2940 GGGTCCCACT GCTCCCCGGG 2850 CCCACGAGCC GGGTGCTCGG ATGGGGGACAC GTTCAACAAA CTGCACAGCA GACGTGTCGT GGATCAGGTA CAAGITGITT 3470 3560 3290 TACCCCTGTG 3380 GAGCCGTCCC Crercrerer 3200 CCTAGTCCAT 3110 GACAGACACA 3020 CTCGGCAGGG TAAAGCACCC ATTTCGTGGG 2930 GAGGCAGAGC CTCCGTCTCG GCAAGCCCCC 2840 CGTTCGGGGG CACCTCAAGG GTGGAGTTCC TCGCACCCGC 3370 GCCCAGACCC CGGGTCTGGG CCCGGGCGAA GGGCCCGCTT GCCCCCGTAC AGCGTGGGCG AGCCCCTGGG 3280 CGGGGGCATG AGGGGCTGCC TCCCCGACGG TCGGGGGACCC 3190 TGGCATGAGG ACCGTACTCC 3010 AGCATGGAAA TCGTACCITT 3100 GCGACGGCCG 2920 מפכתפככ 2830 CCCCACGCGG CACACACTCA GGGGTGCGCC CTGCCCAGCC GACGGGTCGG CGGAGCCTCA GCCTCGGAGT 3360 GTGTGTGAGT 3450 GTACGGGTGA CCCGAGTCGG AAGCCCTAGG TTCGGGATCC CATGCCCACT 3270 GGGCTCAGCC CTCCGGACTC ეეენენტნეე GAGGCCTGAG 3180 2910 3000 3090 GTAAATGAGT CATTTACTCA 2820 CCCCCACGAG GGGGGTGCTC GATGCCCACA CGGAGTGTGT CCTGGCTGCC GGACCGACGG CTACGGGTGT GCCTCACACA 3350 TCCCGACCTC AGGGCTGGAG 3260 GGGCCACGGG GGGATCCCAC CCCGGTGCCC 3170 2990 CCCTAGGGTG TACATACTIC GGCCGAGTCT CCGGCTCAGA ATGTATGAAG 3080 CTGTCTCCGG GACAGAGGCC CGGACACAGG GCCTGTGTCC ACACGTGCAC CCGTGATTGG GACTGGTGCA Tergcacere GGCACTAACC CTGACCACGT 3430 GCCCCTGTCC CGGGGACAGG 3340 GCCCTGGGCT CGGGACCCGA ACGGACCCGG 3070 CCACGGGTCA GGTGCCCAGT Teceredece GTACCCCCTG CATGGGGGAC GAGCCTCTCC CTCGGAGAGG

TCCTAGCGTG

AACTGCCGTT

TIGACGGCAA

CGCGCCAAAC

GCTGCGATTT

ACAGCTCAGG

AAAAGCTTGG

GGCTTTTGCA

TGGAGGCCTA

GAGGCTTTTT CTCCGAAAAA

4350

4340

CCGAAAACGT

TTTTCGAACC

TGTCGAGTCC

4380

4370

AAGTAGTGAG

GCTATTCCAG

CGGCCTCTGA

CTCCGGCGGA

GAGGCCGCCT

TGCAGAGGCC

TTTTTTTT

CGGGGTACCG ACTGATTAAA AAAATAAAT

GCCCCATGGC TGACTAATTT

CCCATTCTCC

CGATAAGGTC TTCATCACTC

16/53

FIG. 14E

Primary Sequence = SEQ ID NO:10 Complementary Sequence = SEQ ID NO:28

4230 CCCAGTTCCG GGATTGAGGC GGGTCAAGGC 3870 CATTCTATTC 3960 ATGGCTTCTG TACCGAAGAC GTTACGCGCA CAATGCGCGT CCTCTCAAAA GGAGAGTTTT GTAAGATAAG TGGCCCACTT ACCEGETGAA CCCGTGCCTT GGGCACGGAA CCTAACTCCG GTTCGCCGGG GGGTGTGGTG CCCACACCAC CANGCGGCCC 3950 GGTGGGCTCT CCACCCGAGA GAGTAGGTGT CTCATCCACA TTGCCCCTCC AACGGGGAGG TCCCTGGCCC AGGGACCGGG 3860 4210 CCATCCCGCC 4120 TTCTCGCCAC AAGAGCGGTG GGTAGGGCGG GTAGACAACA CTGGGGATGC GACCCCTACG TAAGCGCGGC ATTCGCGCCG CGCATTGTCT CTTTAACGTA GCGTAACAGA GGTGCAGTGC 3940 3850 4030 CCACGTCACG 3760 CATCIGITGI 3670 AAGGGAAGGA CTAACTCCGC AGCGGCGCAT TCGCCGCGTA TICCCTICCT 4200 GATTGAGGCG 4290 AGCAGGCATG TCGTCCGTAC 4110 GAMATTGCAT 4020 GICGGAGCIG ACACGGAAGA ICAACGGICG 3840 3930 CCTAGIGIGI AGTTGCCAGC GGATCACACA TCAGGGCGGG AAAGCGAAAG AGTCCCGCCC CGCGCCCTGT GCGCGGGACA TTTCGCTTTC 4190 GGAAGACAAT CCTTCTGTTA 4010 4100 ATAAAATGAG TATTTACTC 3920 TGTGCCTTCT 3830 GTGTGTGTCC CACACACAGG 3740 CAGCAACCAT GICCITGGIA GCGGGCGAGG 4180 4270 CGCCCGCTCC GGGAGGATTG CCCTCCTAAC GGTATCCCCA CCATAGGGGT 4090 TCCTTTCCTA AGGAAAGGAT 3910 CAGCCTCGAC AGCCGCCACA TCGGCGGTGT 3820 CTCAATTAGT TCGCGGGATC 4170 GAGTTAATCA 4260 AGCGCCCTAG GGCTCTAGGG CCGAGATCCC CAGGACGGAT ACTCCCACTG TGAGGGTGAC GACAGCAAGG CTGTCGTTCC 3900 3990 Greceeree CACGGGGACG GTCCTGCCTA 3810 AAGCATGCAT TTCGTACGTA 4160 GGTGGGGCAG TACACTTGCC ATGTGAACGG CCACCCGTC AACCAGCTGG TTGGTCGACC GGGAAGGGAC CCTTCCACGG GGAAGGTGCC 4070 CCCTTCCCTG TCTCACAAGG GGTCGGGAGG AGAGTGTTCC AAGGGAAAAA TYCCCTTYTY GCGTGACCGC CGCACTGGCG AGGCGGAAAG TCCGCCTTTC CCTTGACCCT GGAACTGGGA TegegggTGG ACCCCCACC CCCAGTGCCG GGGTCACGGC CCAGCCCTCC

pD17-cJ-dCH2.H1

ATTGGCAAGA TAACCGTTCT TTTATACCCC AAATATGGGG CCGTGTCCCA GGCACAGGGT AGTACCAAGC TGGTAACTTG ACGTAGCAGC TGCATCGTCG ACCATTGAAC TCATGGTTCG 4450 GGGCGACGGT CCCGCTGCCA GGATTTTATC CCTAAAATAG AAGGCTGGTA TTCCGACCAT

FIG. 14F Primary Sequence = SEQ ID NO:10 Complementary Sequence = SEQ ID NO:28

4860

4850

4840

4830

4820

4810

ACAAGGATCA TGTTCCTAGT

ACTCTTTGTG

GCCACCTTAG

AATCAACCAG TIAGTIGGIC

GGAAGCCATG

CCTTCGGTAC

GACAAATGGT

CCTCCGTCAA

GGAGGCAGTT

TTGGATAGTC AACCTATCAG

ATCTGTACCA

TAGACATGGT

4790

CTGTTTACCA

CGGTGGAATC

TGAGAAACAC

CTCTCTGAGG GAGAGACTCC

CCCAGGCGTC GGGTCCGCAG

TCCCAGAATA AGGGTCTTAT

ATATTTGAAG

TATABACTIC

TTTGGGGAAA AAACCCCTTT

CAGAAATTGA GTCTTTAACT

ACGITITICC TGCARAAGG

TGAAAGTGAC ACTITCACTG

ACGTCCTTAA

TGCAGGAATT

4920

4910

4900

4890

4880

4940

5130

5120

5110

5100

5090

5080

5070

5060

TGACATAATT

TTCTGTGGTG

AAGACACCAC ACTGTATTAA

CCTTGGAATG

GGAACCTTAC

TCTTTGTGAA

GCTTTAGATC

ACTITIGCIG TGAAAACGAC

AGACCATGGG TCTGGTACCC

CATTTTATA

TAAAGCTATG

CGAAATCTAG AGAAACACTT

5040

GCTCCCCTCC CGAGGGGAGG

GTTCAAGAGA

CAAGITCICI

AAGATGCTTT TTCTACGAAA

GACTAACAGG CTGATTGTCC

CGAGAAGAAA GCTCTTCTTT

TTGAAGTCTA

AAGTATAAGT

AAAAGGCATC

TCCAGGAGGA AGGTCCTCCT

TTTCCGTAG

4990

TTCATATTCA AACTTCAGAT

5020

5010

5000

AGGACTITCC TCCTGAAAGG ATTAACAAAC TAATTGTTTG CAGAAGAAAT GICTICTITA CTTCTGGGGT GATGACTAAG GACAAAACGA GAAGACCCCA CTACTGATTC 5300 CIGITITICI 5390 5210 ACTCCTTTTG GAGAAAGGTA CTCTTTCCAT TGAGGAAAAC 5380 ATGTGTTAAA TACACAATTT 5200 GITITITICIT Chararangar TAAGTGTATA ATTCACATAT ATGCCTTTAA TACGGAAATT 5190 GAGAGTTGTA AGATGAGGAG GGATGICICI AAATITCGAG ATICCATITA TATITIAAA TCTACTCCTC ATAAAATTT CAGTGGTGGA GTCACCACCT 5360 5270 5180 CTCTCAACAT TGAATGGGAG TAAGGIAAAT ACTTACCCTC 5170 GATGACGACT CTACTGCTGA ATGGAACTGA TACCTIGACT TTTAAAGCTC 5250 5160 CTACTACTCC GATGATGAGG ATTCCAACCT TAAGGTTGGA CCTACAGAGA GTAAAAATAT 5240 5150 CGGTAGATCA GCCATCTAGT TGTATTTAG ACATAAAATC CCTGTTTGAT GGACAAACTA ATTTCGATAC

pD17-cJ-dCH2.H1

AAACAGAATC

TTTGTCTTAG

TCACCTTCCA AGTGGAAGGT

GTTGGAGAAG

CATGAAGGTT TCTTACTGGT

CAACCTCTTC

AGAATGACCA

GTACTTCCAA

ACCAGTTCAA TGCTCAAGTT

CCGCTCAGGA GGCGAGTCCT

ACCCTGGCCT

ACGGAGACCT

4520

TGCCTCTGGA TGGGACCGGA

4570

TATAGTICIC AGTAGAGAAC

TCATCTCTTG

ATATCAAGAG

TGTCTTAATT

ACAGAATTAA

CCTTTAAAGG

4650

GGAMATTTCC

CITCITIAGCI

GAAGAATCGA 4640

CCATTCCTGA

ACCTGGTTCT TGGACCAAGA

CCCATCCTTT

ACCACTAATA TGGTGATTAT

GGGTAGGAAA

4630

GGTAAGGACT

GCAAGTAAAG CGTTCATTTC

4760

4750

4740

TIATTGAACA ACCGGAATTG

GCCTTAAGAC

TTTGGATGAT

TTGCCAAAG

GCTCATTTC

TGGTGCTCCT

AGTITCTIGG TCAAAGAACC

ACCACGAGGA

4690

4710

TGGCCTTAAC

AATAACTTGT

CGAGTAAAAG AACGGTTTTC AAACCTACTA CGGAATTCTG

FIG. 14G Primary Sequence = SEQ ID NO:10 Complementary Sequence = SEQ ID NO:28

5760

5750

5740

5730

5720

TTAATAAGGA

TGTAAAGGGG

CITITIAATT

GTACCTTTAG

CAAAAATTGT

5640

5630

5620

GAAAATTAA ACATTTCCCC

GITITIAACA CAIGGAAATC

ATTGATACGA

TAACTATGCT

CTGCTATTAA GACGATAATT

5600

GTATCTCACA CATAGAGTGT

TCCACACAGG AGGTGTGTCC

AATTATTCCT

CTCCCACACC GAGGGTGTGG

TTTAAAAAC

TTTTACTIGG

TTTGTAGAGG

CCATACCACA

GGTATGGTGT AAACATCTCC

AGTATTAGTC

ATATCACGGA ACTGATCTCT

TATAAACTAC

ATATTTGATG

TCATAATCAG

TGACTAGAGA

TATAGTGCCT

5700

5690

AAAATGAACG AAATTTTTTG

AGCAATAGCA TCGTTATCGT

AATGTTTATT

GAATATTACC

CITATAATGG

TTTATTGCAG

5820

AAATAACGTC

ACAATTGAAC

GITTAACAACA

CAATTGTTGT

AAAATGAATG TTTTACTTAC

CCTGAAACAT

receeran AGGGGGACTT

GGACTTTGTA

TGTTAACTTG

5810

5800

5790

5780

TTACABATAA

5940

GICTGGAICG CAGACCTAGC

TAGAATAGTA

ATCITATOAT

TCATCAATGT AGTAGTTACA

AACAGGTTTG

TTGTCCAAAC

TAGTIGIGGT ATCAACACCA

CACTGCATIC 1

5910

5900

5890

5880

GCATTTTTT CGTAAAAAA

CACAAATAAA GTGTTTATTT

TCACAAATTT AGTGTTTAAA

5920

6030

6020

6010

6000

5990

5980

TACAAATAAA

TTATAATGGT

TTATTGCAGC

CCCAACTIGT

CTTCGCCCAC GAAGCGGGTG

TGCTGGAGTT ACGACCTCAA

CCCCTAGAGT

GGGGATCTCA

CCTCCAGCGC GGAGGTCGCG

GCTGGATGAT

CGACCTACTA

5960

GGGTTGAACA AATAACGTCG AATATTACCA ATGTTTATTT

6110

6100

TCACTGCCCG AGTGACGGGC TCAACACCAA ACAGGTTTGA GTAGTTACAT AGAATAGTAC ACAATTCCAC TGTTAAGGTG TCTTATCATG CACTCGATTG AGTGTAATTA ACGCAACGCG TTATCCGCTC ACACTTTAAC AATAGGCGAG TGCGTTGCGC CATCAATGTA GIGAGCIAAC ICACATIAAI TGTGAAATTG TGTCCANACT 6280 GACAAAGGAC CATITITIC ACTGCATICI AGIIGIGII CTGTTTCCTG 6270 0609 6180 TGCCTAATGA GTAAAAAAG TGACGTAAGA TGGCGTAATC ATGGTCATAG TICGGACCCC ACGGATTACT TACCAGTATC 6170 6080 ACCGCATTAG ACAACATACG AGCCGGAAGC ATAAAGTGTA AAGCCTGGGG 6250 6070 6160 TETTETATEC TCGGCCTTCG TATTTCACAT CAGCTGGAGA TCGATCTCGA AGCTAGAGCT ACAAATAAAG TGTTTATTTC 0909 6150 6240 Gregaceter CACAAATTTC GTGTTTAAG 6230 6140 AGACATATGG ICTGIAIACC GCAATAGCAT CGTTATCGTA

pD17-cJ-dCH2.H1

AAAAGCTGC

ACCACAAAGG

TGCTATTTAC

TIGCTIGCTI

AATAGAACTC

TGTGTTTAGT

5440

5430

5420

GATTCAAAAA ACTCAGTACG ACACAAATCA

TGAGTCATGC

CTAAGTTTT

AAGTCTTAAC TTCAGAATTG

5460

TIAICTIGAG AACGAACGAA ACGATAAATG IGGIGITICC

TTTTCGACG

TTTTTTTAC

AACATACTGT

TTATAATCAT

GGCATAACAG

TTTATARGTA AAATATTCAT

TTCTGTAACC

TGGAAAATA

AAGAAAATTA

ACTGCTATAC

5520

5510

TGACGATATG TICITITAAT ACCITITIAT AAGACATIGG

5540

5530

5560

TTGTATGACA AAAAAGAATG

CCGTATTGTC AATATTAGTA

FIG. 14H Primary Sequence = SEQ ID NO:10 Complementary Sequence = SEQ ID NO:28

6750

6740

6730

6660

6570

GCGTTTTTCC

CCCCTTCCTC

GTAAAAAGGC CATTTTCCG

GCCAGGAACC

CCAGCAAAAG

GAGCAAAAGG

TTCTTGTACA

AAGAACATGT

TAACGCAGGA

ATTGCGTCCT

AATCAGGGA TTAGTCCCCT

6540

6530

6520

6510

TTATCCACAG

GGTAATACGG

ACTCAAAGGC TGAGTTTCCG

GTATCAGCTC

GCGGCGAGCG

AGCAAGCCGA

GACGCGAGCC

GTGACTGAGC

GAAGGAGCGA

CTTCCTCGCT

6410 CACTGACTCG

CIGCGCICGG

TCGTTCGGCT

6440

6430

6420

6470

6460

6450

CGCTCTTCCG

CGCATAACCC

GCGTATTGGG

GAGGCGGTTT

CGCGCGGGGA

AATCGGCCAA

TGCATTAATG

AGCACGGTCG

GGGAAACCTG

CTTTCCAGTC

GAAAGGTCAG

TCGTGCCAGC

6340

6330

6360

TACCAGGCGT

ATGGTCCGCP

TGATATTTCT

ACTATAAAGA

ACCCGACAGG TGGGCTGTCC

AGGTGGCGAA

CTCAAGTCAG

AAAATCGACG TTTTAGCTGC

GAGCATCACA

CCCCCCTGAC

ATAGGCTCCG TATCCGAGGC

CTCGTAGTGT

6640

6630

6620

6610

6600

6590

GGAAGCGTGG

TCTCCCTTCG

TGTCCGCCTT

ACCEGATACC

TGGCCTATGG ACAGGCGGAA

GGACGCCGAA

CCTGCCGCTT

CTGTTCCGAC

GTGCGCTCTC

AAGCTCCCTC

Trecected

AAGGGGGGACC

TTCGAGGGAG

0699

6840

CCCGTTCAGC

GCACGAACCC

TGGGCTGTGT

COCTCCAAGC

GTAGGTCGTT

TCAGTTCGGT

TGTAGGTATC

ACATCCATAG AGTCAAGCCA

TACGAGTGCG

ATGCTCACGC

CCCTTTCTCA

6820

6810

6800

6790

6780

CGTGCTTGGG

6930

actggtaaca Tgaccattgt

GGCAGCAGCC

TATCGCCACT

AGACACGACT TCTGTGCTGA

GTTGGGCCAT

CAACCCGGTA

GTCTTGAGTC

GGTAACTATC

CGCCTTATCC

CCGACCGCTG

0989

CCATTGATAG

6910

6900

6890

6880

TITITCCIAG AGIICITCIA GGAAACIAGA AAAGAIGCCC CAGACIGCGA GICACCIIGC CAGTGGAACG 7110 CCACCAAAAA GTATTTGGTA CATABACCAT GGTGGTTTTT GTCTGACGCT TAGAAGGACA CGCTGGTAGC GCGACCATCG ATCTTCCTGT TTTCTACGGG AACAAACCAC TGCCGATGTG ACGGCTACAC 7090 TTGTTTGGTG CCTTTGATCT TGATCCGGCA TGGCCTAACT ACCCCATTGA 7080 ACTAGGCCGT 7170 6990 AAAAAGGATC TCAAGAAGAT TGGTAGCTCT CTTTTTCTCA ACCATCGAGA 7160 GRACTICACC CTTGAAGTGG 7070 6980 GAAAAAGAGT GATGTCTCAA CTACAGAGTT 7060 7150 6970 ACGCGCAGAA CGICGICIAA IGCGCGICII GTTACCTTCG 7140 CATCCGCCAC CAATGGAAGC GTAGGCGGTG 7050 6960 GCAGCAGATT 7130 AGCGAGGTAT GCTGAAGCCA CGACTTCGGT 6950 TCGCTCCATA 7040 AGACGCGAGA TTGTTTGCAA AACAAACGTT GGATTAGCAG TCTGCGCTCT CCTAATCGTC

GGCGACAACT

TTCCTAGAAT

CTTTTGAGAG

20/53

FIG. 14I

Primary Sequence = SEQ ID NO:10 Complementary Sequence = SEQ ID NO:28

TTTACTITCA B010 GGTTGACTAG AAGTCGTAGA AAATGAAAGT ACCITITIGGA AGAAGCCCCG CGGCGACCGA TCTTCGGGGC 7740 7560 ACAGGCATCG TTGTGCAAAA AACACGTTTT CIGCATAATT GACGTATTAA GCCGCTGGCI TCCGCCTCCA TGTCCGTAGC AGGCGGAGGT TTTCGTTCAT CCGCGAGACC GGCGCTCTGG TTTABATCAR TITIACTICA AAAITIAGII NAGCARGIA TGGAAAACGT TTCAGCATCT ATAGTGTATG TATCACATAC ACGGTAACGA ATCCCCCATG TAGGGGGTAC TATGGCAGCA ATACCGTCGT TGCCATTGCT 8000 TGCAACTTTA ACGTTGAAAT CTAGACAGAT 7730 TGCAATGATA ACGITACTAT AAAATGAAGT 7370 GATCTGTCTA TGCTCATCAT CCAACTGATC 8080 CACTCATGGT GTGAGTACCA GTAAGACTCT 7990 ACGAGTAGTA CGTTGCAACA GAGTTACATG CTCAATGTAC CATTCTGAGA GCAACGTTGT CTTCACCAGG 7720 GATAGAGTCG GCCCCAGTGC CGGGGTCACG 7540 GAAGTGGTCC 7450 TTTAATTA CTATCTCAGC AAAATTTAAT 7360 ACTCGTGCAC TGAGCACGTG ACTITARAG TGAAATTTTC AGTIGGTICA GCAGTGTTAT CGTCACAATA TCAACCAAGT 8070 AATAGTTTGC TTATCAAACG CGATCAAGGC GCTAGTTCCG 7800 7890 7530 GCCGAGCGCA CGGCTCGCGT 7620 TTACCATCTG AATGGTAGAC 7710 ATGCTTAATC AGTGAGGCAC TCACTCCGTG 7440 7350 ACCTAGATCC TGGATCTAGG GATGTAACCC CTACATTGGG ACATAGCAGA TGTATCGTCT ACCACTCATG 7970 8060 GCCAAGGGTT TAAGTTGGCC ATTCAACCGG 7880 TGGTGAGTAC CGGTTCCCAA AAGCGGTCAA TTCGCCAGTT 7700 7790 TACGAATTAG TGCCCTCCCG AGCCGGAAGG TCGGCCTTCC 7610 AAGGATCTTC TTCCTAGAAG 7430 ACGGGAGGGC 7340 7250 CTAGGTCAAG GATCCAGTTC AACAGICTIC AAAGACACTG ATACCGCGCC TATGGCGCGG 8050 TTTCTGTGAC 7960 TTGTCAGAAG CATTCAGCTC 7780 7870 TAACTACGAT ATTGATGCTA TAAACCAGCC GAGTAAGTAG CTCATTCATC GTAAGTCGAG ATTIGGICGG 7510 ACAGTTACCA GATTATCAAA CTAATAGTTT 7330 TGTCAATGGT 7420 ATACGGGATA TATGCCCTAT CCGCTGTTGA CATTCTACGA GGAGGCTAGC 7950 8040 7860 GGTATGGCTT CCATACCGAA 7770 CCTCCGATCG GTAAGATGCT TTATCAGCAA CGGGAAGCTA GCCCTTCGAT CAGCACATCT GTCGTGTAGA AATAGTCGTT ACTIGGICTG TGAACCAGAC 7500 7320 7410 AACCAGTACT TTGGTCATGA 7230 AAGGATCTTA CCCGGCGTCA CATGCCATCC GGGCCGCAGT GTACGGTAGG CICCITICGGI 7940 CCGAGGTCTA CICGICGITI GAGGAAGCCA GGCTCCAGAT 7580 TAATTGTTGC ATTAACAACG GAGCAGCAAA 7850 GACTGAGGGG 7490 AATTCCCTAA ATATGAGTAA TATACTCATT CTGACTCCCC TIAAGGGATT 7310 GAMACTCTC GTTGCTCTTG CAACGAGAAC CTCTTACTGT GAGAATGACA AAGCGGTTAG TTCGCCAATC TCCAGTCTAT AGGTCAGATA TGGTGTCACG ACCACAGTGC GTGCGAGTGG CCATAGTTGC GGTATCAACG CACGCTCACC AGATTTCATA AAAACTCACG TCTAAAGTAT TTTTGAGTGC

FIG. 14J
Primary Sequence = SEQ ID NO:10
Complementary Sequence = SEQ ID NO:28

| B190 CTCATACTCT GAGTATGAGA | 8280 AAACAAATAG TTTGTTTATC | |
|--|---|---|
| 8180 ATGTTGAATA TACAACTTAT | 8270 TTAGAAAAT AATCTTTTA | |
| 8170 CGACACGGAA GCTGTGCCTT | 8260 TTGAATGTAT AACTTACATA | |
| B160 GGAATAAGGG CCTTATTCCC | 8250 GGATACATAT CCTATGTATA | |
| 8150 CGCAAAAAG GCGTTTTTC | 8240 TCTCATGAGC AGAGTACTCG | 8330 C G |
| 8140 GGCAAAATGC CCGTTTTACG | 8230 AGGGTTAITG TCCCAATAAC | 8320 CACCTGACGT GTGGACTGCA |
| CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAAATGC CGCAAAAAAG GGAATAAGGG CGACACGGAA ATGTTGAATA CTCATACTCT GGTCGCAAAG ACCCACTCGT TTTTGTCCTT CCGTTTTTACG GCGTTTTTTC CCTTATTCCC GCTGTGCCTT TACAACTTAT GAGTATGAGA | 8280 8250 8250 8280 8280 8280 8280 8280 | 8320 8320 8320 8320 8320 CACCTGACGT CCCCAAGGCG CACATTAAAGGG GCTTTTCACG GTGGACTGCA G |
| 8120 TGGGTGAGCA ACCCACTCGT | 8210 ATATTATTGA TATAATAACT | 8300 CACATTICCC GIGTAAAGGG |
| 8110 CCAGCGTTTC GGTCGCAAAG | 8200 TCCTTTTCA AGGAAAAAGT | 8290 GGGTTCCGCG CCCAAGGCGC |

FIG. 15



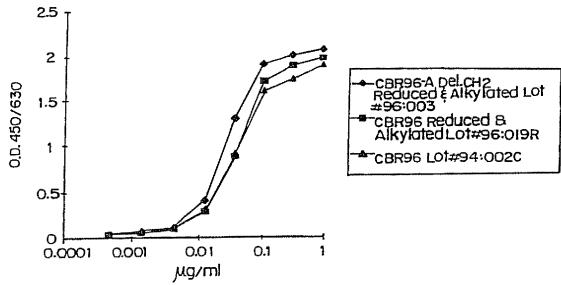


FIG. 16

hBR96-2B:L235 to A235 and G237 to A237

hBR96-2C:E318 to S318, K320 to S320, and K322 to S322

hBR96-2D:P331 to A331

hBR96-2E:L235 to A235, G237 to A237, E318 to S318, K320 to S320, and K322 to S322

hBR96-2F:L235 to A235, G237 to A237, and P331 to A331

hBR96-2G:E318 to S318, K320 to S320, K322 to S322, and P331 to A331

hBR96-2H: L235 to A235, G237 to A237, E318 to S318, K320 to S320, K322 to S322, and P331 to A331

FIG. 17

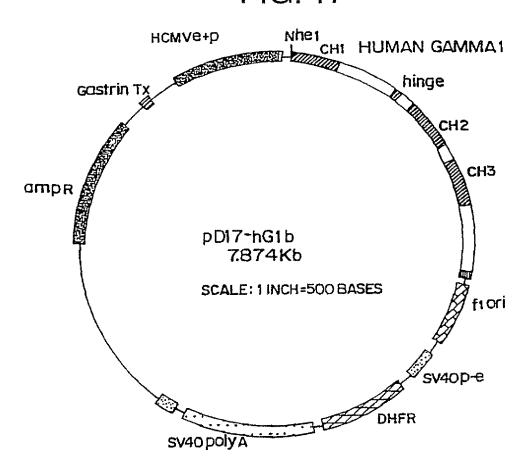


FIG. 18A

(SEQ ID NO:22)

| 51 GGTCAATCGA TTGGAATTCT TGCGGCCGCT TGCTAGCCAC CATGGAGTTG 101 TGGTTAAGCT TGGTCTTCCT TGTCCTTGTT TTAAAAGGTG TCCAGTGTGA 151 AGTGCAACTG GTGGAGTCTG GGGGAGGCTT AGTGCAGCCT GGAGGGTCCC 201 TGCGACTTTC CTGTGCTGCA TCTGGATTCC CGTTCAGTGA CTATTACATG 251 TATTGGGTTC GCCAGGCTCC AGGCAAGGGA CTGGAGTGGG TCTCATACAT 301 TAGTCAAGAT GGTGAATATAA CCGACTATGC AGACTCCGTA AAGGGTCGAT 401 AGCCTGAGGG ACGAGGACAA GCCGTGTAT TACTGTGCAA GAGGCCTGGC 451 GGACGGGGCC TGGTTTGCTT ACTGGGGCCA AGGGACTCTG GTCACGGTCT 501 CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCCC 551 AAGAGCACCT CTGGGGGCAC AGGGGCCTG GGCTGCCTGG TCAAGGACTA 601 CTTCCCCGAA CCGGTGACGG TGTCCTACAGT CTAACCAGCG 651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CTAAGGACTA 701 AGCAGCGTGG TCACCGTGC CTCCAGCAGC CTCCAGGACT CTACTCCCTC 701 AGCAGCGTG AATCACAAGC CACCAAGGC CTCCAGGACT CTACTCCCTC 851 CTGCAACGT AATCACAAGC CAGGAGACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGGAGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCCCAGTC 751 CTGCAACGTG AATCACAAGC CAGGAGACAC CAAGGTGAC AAGAAAGTTG 801 GTGAGGAGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGGCCAGCA 851 CGCTCCTCCC TGGACGCAC CCGGCTTACC CAGGGCCCC AGCACAGCAC | : | l GGTACCAATT | TAAATTGATA | TCTCCTTAGG | TCTCGAGTCT | CIAGATAACC |
|--|------|--------------|------------|------------|------------|------------|
| 151 AGTGCAACTG GTGGAGTCTG GGGGAGGCTT AGTGCAGCCT GGAGGGTCCC 201 TGCGACTTTC CTGTGCTGCA TCTGGATTCC CGTTCAGTGA CTATTACATG 251 TATTGGGTTC GCCAGGCTCC AGGCAAGGGA CTGGAGTGGG TCTCATACAT 301 TAGTCAAGAT GGTGATATAA CCGACTATGC AGACTCCGTA AAGGGTCGAT 351 TCACCATCTC CAGAGACAAT GCAAAGAACA GCCTGTACCT GCAAATGAAC 401 AGCCTGAGGG ACGAGGACAC AGCCGTGTAT TACTGTGCAA GAGGCCTGGC 451 GGACGGGCC TGGTTTGCTT ACTGGGGCCA AGGGACTCTG GTCACGGTCT 501 CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC 551 AAGAGCACCT CTGGGGGCAC AGGGGCCCTGG TCAAGGACTA 601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAAA CTCAGGGCCC CTGACCAGCG 651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CTCAGGGCCC CTGACCAGCG 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG 851 CGCTCCTGCC TGGACCACTC CCGGCTATGC AGCCCTAGGC 951 ATGCTCAGCG AGCACAGGGA GGGAGGGTGT CTGCTGGAAG 901 AGGCAGGGCC CGTCTGCCTC TCCAGCAGC GGCCCCCAGTC 951 ATGCTCAGGG AGAGGGTTT CTGCCTGGC CCCCCACTC 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC CCCCCAGTC 1051 GGCTCAGGCC TGCCAAGAGC CAAGAAGGG GCCCTCTGCC CCCCCCACTC 1051 GCCTCAGCCC AAAGGCCAAA CTCTCCCGC ACACAACGG GCAGGTCTG 1051 GCCTCAGCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTC CCCTGACCCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTC CCCTGACCCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTC CCCTGACCTAC 1121 CTCTCCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT 1220 CTTGTGACAA AACTCACAA TGCCCAACGG TGCCCCAGTCAAGCCCAACCTTCT 1251 CTCTCCCCCCC CCAGCTCAACC TCCCCAGCTCT TCTCTCCCCAGC GCCCCAAACAC 1251 GCCTCGCCCT CCAGCTCAACC TCCCCACTCT TCTCTCCCCAGC GCCCCAAACAC 1251 GCCTCGCCCT CCAGCCCAACAC TGCCCCAACCT TCTCTCCACTC CCTCAGCTCAACC TCTCCCACTC CCTCAGCCCAACCTTCT 1251 CTCTCCCCCCC AAAGGCCAAA CTCTCCCACTC CCTCAGCTCAACCTAACCCCAACCTTCT 1251 CTCTCCCCCCC AAAGGCCAAAC TCCCCCACTCT TCTCTCCACTC CCTCAGCCCAACCTTCT 1251 CTCTCCCCCCC AAACGCCAACA TGCCCCACTGT TCTCTCACCTC CCTCAGCCCAACCTTCT 1251 CTCTCCCCCCC AAACCCAACAC TGCCCCACGTAAC TCCCCACCTAACCTA | 53 | l GGTCAATCGA | TTGGAATTCT | TGCGGCCGCT | TGCTAGCCAC | CATGGAGTTG |
| 201 TGCGACTTC CTGTGCTGCA TCTGGATTCC CGTTCAGTGA CTATTACATG 251 TATTGGGTTC GCCAGGCTCC AGGCAAGGGA CTGGAGTGGG TCTCATACAT 301 TAGTCAAGAT GGTGATATAA CCGACTATGC AGACTCCGTA AAGGGTCGAT 351 TCACCATCTC CAGAGACAAT GCCAAAGAACA GCCTGTACCT GCAAATGAAC 401 AGCCTGAGGG ACGAGGACAC AGCCGTGTAT TACTGTGCAA GAGGCCTGGC 451 GGACGGGGCC TGGTTTGCTT ACTGGGGCCA AGGGACTCTG GTCACGGTCT 501 CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC 551 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA 601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGACCT CTACCAGCG 651 GCGTGCACC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG 851 CGCTCCTGCC TGGACCAGCAC CCAGCACAC CAAGGTGGAC CAGGCACCAGCA 901 AGGCAGGCCC CGTCTGCCTC TCCAGCAGC CCAGGCTCC CAGGCCCAGCA 901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCCCAGTC CAGGCCTCAGCAC 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC CCCCCAGCCC 1051 GGCTCAGACC TGCCAAGAGC CAAGCCCTGC CCCCCACTC 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCCCACTC 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTC CCCCGACCTC 11251 CTCCTCCCAG ATTCCAGTAA CTCCCCATCT TCTCTCTGCA GAGCCCCAATT 1251 CTCCTCCCAG ATTCCAGTAA CTCCCCACTT TCTCTCTCCACGA GGCCCAAATT 1251 CTCCTCCCAG ATTCCAGTAA CTCCCCACTT TCTCTCTCCACCC GACCCCAACTC 1251 CTCCTCCCAG ATTCCAGTAA CTCCCCACTT TCTCTCTCCACG GACCCCCAACTC 1251 CTCTTCCCAGC AAACCCCAAAC TGCCCCACTT TCTCTCTCCACG GCCCCAACTC 1251 CTCTTCCCAG ATTCCAGTAA CTCCCCACTT TCTCTCTCCACG GCCCAACTTCT 1251 CTCTTCCCAG ATTCCAGTAA CTCCCCACTT TCTCTCTCCAC GCCCCAACTCT 1251 CTCCTCCCAG AAACCCCAAAC TGCCCCAACTCT TCTCTCTCCCACG GCCCAAACTCT TCTCTCTCCCACG GCCCAAACTCT TCTCTCTCCACG GCCCAAACTCT TCTCTCTCCACG GCCCAAACTCT TCTCTCTCCACG GCCCAAACTCT TCTCTCTCCACG GCCCAACTCT TCTCTCTCCACG GCCCAAACTCT TCTCTCTCCACTC GCCCAACTCT T | 102 | TGGTTAAGCT | TGGTCTTCCT | TGTCCTTGTT | TTAAAAGGTG | TCCAGTGTGA |
| 251 TATTGGGTTC GCCAGGCTCC AGGCAAGGGA CTGGAGTGGG TCTCATACAT 301 TAGTCAAGAT GGTGATATAA CCGACTATGC AGACTCCGTA AAGGGTCGAT 351 TCACCATCTC CAGAGACAAT GCCAAAGAACA GCCTGTACCT GCAAATGAAC 401 AGCCTGAGGG ACGAGGACAC AGCCGTGTAT TACTGTGCAA GAGGCCTGGC 451 GGACGGGGCC TGGTTTGCTT ACTGGGGCCA AGGGACTCTG GTCACGGTCT 501 CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC 551 AAGAGCACCT CTGGGGGCAC AGGGGCCTG GGCTGCCTGG TCAAGGACTA 601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGGCCC CTGACCAGCG 651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACC AGACCTACAT 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG 851 CGCTCCTGCC TGGACGGAG GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG 851 CGCTCCTGCC TGGACGGAC GCGGAGGGTGT CTGCTGGAAG CCAGGCTCAGC 901 AGGCAGGCCC CGTCTGCCTC TCCACCCGGA GGCCCCAGTC CAGGGCAGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCTTGC CGCCCCAGTC 1051 GGCTCAGACC TGCCAAGAGC CAAGACACC CCCCAGGCTC TGGGCAGGCA 1051 GGCTCAGACC AGAGGGAAGC CATATCCGGG AGACCCTGC CCCCCACTC 1101 AGCCCACCC AAAGGCCAAA CTCTCCACTC CCTCAGCTC CCCTGACCTAC 11251 CTCCTCCCAG ATTCCAGTAA CTCCCCAATCT TCTCTCTGCA GACCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCAAAT 1251 CTCCTCCCAG ATTCCAGCA TGCCCACCGT GCCCAGGTAA GCCAGCCCAA | 151 | AGTGCAACTG | GTGGAGTCTG | GGGGAGGCTT | AGTGCAGCCT | GGAGGGTCCC |
| 301 TAGTCAAGAT GGTGATATAA CCGACTATGC AGACTCCGTA AAGGGTCGAT 351 TCACCATCTC CAGAGACAAT GCAAAGAACA GCCTGTACCT GCAAATGAAC 401 AGCCTGAGGG ACGAGGACAC AGCCGTGTAT TACTGTGCAA GAGGCCTGGC 451 GGACGGGCC TGGTTTGCTT ACTGGGGCCA AGGGACTCTG GTCACGGTCT 501 CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCCC 551 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA 601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGGCCC CTGACCAGCG 651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG 851 CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCCAGCA 901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGCA 1001 CAGGCTAGGC TGCCAAGAGC CAGGCCCTGC ACACAAGAGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTGC CCCTGACCTTC 1251 CTCCTCCCAG ATTCCAGCAA CTCTCCACTC CCTCAGCTCG GACCACCTTCT 1251 CTCCTCCCAG ATTCCAGCAA CTCTCCACTC CCTCAGCTCG GACCACCTTCT 1251 CTCCTCCCAG ATTCCAGCAA CTCTCCACTC CCTCAGCTCAG | 201 | TGCGACTTTC | CIGIGCIGCA | TCTGGATTCC | CGTTCAGTGA | CTATTACATG |
| 351 TCACCATCTC CAGAGACRAT GCARAGAACA GCCTGTACCT GCARATGARC 401 AGCCTGAGGG ACGAGGACAC AGCCGTGTAT TACTGTGCAA GAGGCCTGGC 451 GGACGGGCC TGGTTTGCTT ACTGGGGCCA AGGGACTCTG GTCACGGTCT 501 CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC 551 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA 601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGGCCC CTGACCAGGG 651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAAGTTG 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG 851 CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA 901 AGGCAGGCCC CGTCTGCCT TTCACCCGGA GGCCTCTGCC CGGCCCACTC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 101 AGCCCACCC AAAGGCCAAA CTCTCCACTC CCTCAGCTGC GACCACCTTC 1251 CTCCTCCCAG ATTCCAGGAA CTCTCCACTC CCTCAGCTCG GACCACCTTCT 1251 CTCCTCCCAG ATTCCAGCA TGCCCAACCT TCTCTCTCTCAGG GACCCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCCT GCCCAGGTAA GCCCAAGATA GCCCAACATCT 1251 CTCCTCCCAG ATTCCACCAC TGCCCACCCT GCCCAGGTAA GCCCAACATCT 1251 CTCCTCCCAG ATTCCACCAC TGCCCACCCT GCCCAGGTAA GCCCAACAT 1251 CTCCTCCCAG ATTCCACCAC TGCCCACCCT GCCCAGGCCAACT 1251 CTCCTCCCAG ATTCCACCAC TGCCCACCCT GCCCAAGCCCAACT TCTCTCTCCCAG GCCCCAACT TCTCTCTCCAGC TACCCAGCCCAACT TCTCTCTCCAG GCCCAACCTTCT TCTCTCTCCAG GACCCCAACT 1251 CTCCTCCCAG ATTCCACCAC TGCCCACCCT GCCCAAGGTAA GCCCAAGCTTCT TCTCTCTCCAG GACCCCAAACT TCTCTCCACCC GCCCAAGCCCAACT TCTCTCCACCC GCCCAAGCCCAACT TCTCTCCACCC GCCCCAACCT TCTCTCTCCAGC TACCCCACCCT GCCCAACCT TCTCTCTCCAGC TACCCCACCCT GCCCAACCT TCTCTCTCTCCAG GCCCAACCT TCTCTCTCCAGC TACCCCACCC GCCCCAACT TCTCTCCACCC GCCCCAACT TCTCTCTCTCAACC TCCCAACCT TCTCTCTC | 251 | . TATTGGGITC | GCCAGGCTCC | AGGCAAGGGA | CIGGAGIGGG | TCTCATACAT |
| 401 AGCCTGAGGG ACGAGGACAC AGCCGTGTAT TACTGTGCAA GAGGCCTGGC 451 GGACGGGGCC TGGTTTGCTT ACTGGGGCCA AGGGACTCTG GTCACGGTCT 501 CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC 551 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA 601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGGCCC CTGACCAGCG 651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGGCTCAG 851 CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA 901 AGGCAGGCCC CGTCTGCCTC TTCACCCCGA GGCCCTGCC CGCCCCACTC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCCAGGCTC TGGGCAGGCA 1001 CAGGCTAGGC GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1251 CTCCTCCCAG ATTCCAGTAA CTCCCCAATCT TCTCTCTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGGTAA GCCAGCCCAG | 301 | TAGTCAAGAT | GGTGATATAA | CCGACTATGC | AGACTCCGTA | AAGGGTCGAT |
| 451 GGACGGGCC TEGTTTGCTT ACTGGGCCCA AGGGACTCTG GTCACGGTCT 501 CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC 551 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA 601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGGCCC CTGACCAGCG 651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGGGCCC AGCACAGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG 851 CGCTCCTGCC TGGACGACAC CAGGTGGAC CAGGCTCAGC 901 AGGCAGGCCC CGTCTGCCTC TCCACCGGA GGCCCCAGTC CAGGCCACCC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTC GACACCTTCT 1251 CTCCTCCCAG ATTCCAGTAA CTCCCCAATCT TCTCTTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG 1251 GCCTCGCCCT CCAGGCCCT GCCCAGGCTA GCCAGCCCAG | 351 | TCACCATCTC | CAGAGACAAT | GCAAAGAACA | GCCTGTACCT | GCAAATGAAC |
| SOI CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC 551 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA 601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG 651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGGGCCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG 851 CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA 901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTC GACACCCTTCT 1251 CTCCTCCCAG ATTCCAGTAA CTCCCCAATCT TCTCTCTGCA GACCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG 1251 GCCTCGCCCT CCAGCTCAAC TGCCCACCGT GCCCAGGTAA GCCAGCCCCAG 1251 GCCTCGCCCT CCAGCTCAAC TGCCCACCGT GCCCAGGTAA GCCAGCCCCAG 1251 GCCTCGCCCT CCAGCTCAAG TGCCCACCGT GCCCAGGTAA GCCAGCCCCAG | 401 | AGCCTGAGGG | ACGAGGACAC | agccgtgtat | TACTGTGCAA | GAGGCCTGGC |
| 551 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA 601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG 651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG 851 CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA 901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTG GACACCTTCT 1251 CTCCTCCCAG ATTCCAGTAA CTCCCCACTC TCTCAGCTG GACACCTTCT 1251 CTCCTCCCAG ATTCCAGTAA CTCCCCACTG GCCCAGGTAA GCCCAGCCAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCCAGCCAG | 451 | GGACGGGGCC | TGGTTTGCTT | ACTGGGGCCA | AGGGACTCTG | GTCACGGTCT |
| 601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG 651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG 851 CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA 901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCTTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1251 CTCCTCCCAG ATTCCAGTAA CTCCCCAATCT TCTCTCTGCA GAGCCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGGCCAG | 501 | CITCCGCTAG | CACCAAGGGC | CCATCGGTCT | TCCCCCTGGC | ACCCTCCTCC |
| 651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG 851 CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA 901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1151 CTCCTCCCAG ATTCCAGTAA CTCCCCAATCT TCTCTCTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCCAGGCCAG 1251 GCCTCGCCCT CCAGCCCTG CCCAGGCCTG TAGCCCAGCTA | 551 | AAGAGCACCI | CTGGGGGCAC | AGCGGCCCTG | GGCTGCCTGG | TCAAGGACTA |
| 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG 851 CGCTCCTGCC TGGACGCATC CCAGCTATGC AGCCCCAGTC CAGGGCAGCA 901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1151 CTCCTCCCAG ATTCCAGTAA CTCCCCAATCT TCTCTCTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG | 601 | CITCCCCGAA | CCGGTGACGG | TGTCGTGGAA | CTCAGGCGCC | CTGACCAGCG |
| 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG 851 CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA 901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1251 CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG 1251 GCCTCGCCCT CCAGCTCAG GCCGGGACAGG TGCCCTAGAG TAGCCTGCAT | 651 | GCGTGCACAC | CITCCCGGCI | GTCCTACAGT | CCTCAGGACT | CTACTCCCTC |
| 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTGAG 851 CGCTCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA 901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCCAGGCTC TGGGCAGGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGGCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1151 CTCCTCCCAG ATTCCAGTAA CTCCCCAATCT TCTCTCTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG 1251 GCCTCGCCCT CCAGCTCAAG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT | 701 | AGCAGCGTGG | TCACCGTGCC | CTCCAGCAGC | TTGGGCACCC | AGACCTACAT |
| 851 CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA 901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1151 CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG 1251 GCCTCGCCCT CCAGCTCAGG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT | 751 | CIGCAACGIG | AATCACAAGC | CCAGCAACAC | CAAGGTGGAC | AAGAAAGTTG |
| 901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1251 CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG 1251 GCCTCGCCCT CCAGCTCAAG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT | 801 | GTGAGAGGCC | AGCACAGGGA | GGGAGGGTGT | CTGCTGGAAG | CCAGGCTCAG |
| 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGGCA 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGG CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1251 CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG 1251 GCCTCGCCCT CCAGCTCAAG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT | 851 | CGCTCCTGCC | TGGACGCATC | CCGGCTATGC | AGCCCCAGTC | CAGGGCAGCA |
| 1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1151 CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG 1251 GCCTCGCCCT CCAGCTCAAG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT | 901 | AGGCAGGCCC | CGTCTGCCTC | TTCACCCGGA | GCCTCTGCC | CGCCCCACTC |
| 1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA 1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1151 CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG 1251 GCCTCGCCCT CCAGCTCAAG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT | 951 | ATGCTCAGGG | AGAGGGTCTT | CTGGCTTTTT | CCCCAGGCTC | TGGGCAGGCA |
| 1101 AGCCCACCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1151 CTCCTCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG 1251 GCCTCGCCCT CCAGCTCAAG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT | 1001 | CAGGCTAGGT | GCCCCTAACC | CAGGCCCTGC | ACACAAAGGG | GCAGGTGCTG |
| 1151 CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT 1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG 1251 GCCTCGCCCT CCAGCTCAAG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT | 1051 | GGCTCAGACC | TGCCAAGAGC | CATATCCGGG | AGGACCCTGC | CCCTGACCTA |
| 1201 CITGIGACAA AACTCACACA TGCCCACCGI GCCCAGGIAA GCCAGCCCAG 1251 GCCTCGCCCI CCAGCTCAAG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT | 1101 | AGCCCACCCC | AAAGGCCAAA | CTCTCCACTC | CCTCAGCTCG | GACACCTTCT |
| 1251 GCCTCGCCCT CCAGCTCAAG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT | 1251 | CTCCTCCCAG | ATTCCAGTAA | CTCCCAATCT | TCTCTCTGCA | GAGCCCAAAT |
| | 1201 | CITGIGACAA | AACTCACACA | TGCCCACCGT | GCCCAGGTAA | GCCAGCCCAG |
| 1301 CCAGGGACAG GCCCCAGCCG GGTGCTGACA CGTCCACCTC CATCTCTTCC | 1251 | GCCTCGCCCT | CCAGCTCAAG | GCGGGACAGG | TGCCCTAGAG | TAGCCTGCAT |
| | 1301 | CCAGGGACAG | GCCCCAGCCG | GGTGCTGACA | CGTCCACCTC | CATCTCTTCC |

FIG. 18B (SEQ ID NO:22) 235 237

| | | 235 | 237 | | |
|------|--------------|-------------------|-----------------------|------------|------------|
| 1351 | TCAGCACCTG | AACTCCTGGG | GGGACCGTCA | GTCTTCCTCT | TCCCCCAAA |
| 1401 | ACCCAAGGAC | ACCCTCATGA | TCTCCCGGAC | CCCTGAGGTC | ACATGCGTGG |
| 1451 | LTGGTGGACGT | GAGCCACGAA | GACCCTGAGG | TCAAGTTCAA | CTGGTACGTG |
| 1501 | GACGGCGTGG | AGGTGCATAA | TGCCAAGACA | AAGCCGCGGG | AGGAGCAGTA |
| 1551 | CAACAGCACG | TACCGTGTGG | TCAGCGTCCT | CACCGTCCTG | CACCAGGACT |
| 1601 | GGCTGAATGG | 318 CAAGGAGTAC | 320 322 AAGTGCAAGG | TCTCCAACAA | AGCCCTCCCA |
| 1651 | GCCCCCATCG | AGAAAACCAT | CTCCAAAGCC | AAAGGTGGGA | CCCGTGGGGT |
| 1701 | . GCGAGGGCCA | CATGGACAGA | GCCGCCTCG | GCCCACCCTC | TGCCCTGAGA |
| 1751 | . GTGACCGCTG | TACCAACCTC | TGTCCCTACA | GGGCAGCCCC | GAGAACCACA |
| 1801 | . GGTGTACACC | CTGCCCCCAT | CCCGGGATGA | GCTGACCAAG | AACCAGGTCA |
| 1851 | GCCTGACCTG | CCTGGTCAAA | GGCTTCTATC | CCAGCGACAT | CGCCGTGGAG |
| 1901 | TGGGAGAGCA | ATGGGCAGCC | GGAGAACAAC | TACAAGACCA | CGCCTCCCGT |
| 1951 | GCTGGACTCC | GACGGCTCCT | TCTTCCTCTA | CAGCAAGCTC | ACCGTGGACA |
| 2001 | . AGAGCAGGTG | GCAGCAGGGG | AACGTCTTCT | CATGCTCCGT | GATGCATGAG |
| 2051 | GCTCTGCACA | ACCACTACAC | GCAGAAGAGC | CTCTCCCTGT | CTCCGGGTAA |
| 2101 | . ATGAGTGCGA | CGGCCGGCAA | GCCCCGCTC | CCCGGGCTCT | CGCGGTCGCA |
| 2151 | CGAGGATGCT | TGGCACGTAC | CCCCTGTACA | TACTTCCCGG | GCGCCCAGCA |
| 2201 | TGGAAATAAA | GCACCCAGCG | CTGCCCTGGG | CCCCTGCGAG | ACTGTGATGG |
| 2251 | TTCTTTCCAC | GGGTCAGGCC | GAGTCTGAGG | CCTGAGTGGC | ATGAGGGAGG |
| 2301 | CAGAGCGGGT | CCCACTGTCC | CCACACTGGC | CCAGGCTGTG | CAGGTGTGCC |
| 2351 | TGGGCCCCCT | AGGGTGGGGC | TCAGCCAGGG | GCTGCCCTCG | GCAGGGTGGG |
| 2401 | GGATTIGCCA | GCGTGGCCCT | CCCTCCAGCA | GCACCTGCCC | TGGGCTGGGC |
| 2451 | CACGGGAAGC | CCTAGGAGCC | CCTGGGGACA | GACACACAGC | CCCTGCCTCT |
| 2501 | GTAGGAGACT | GTCCTGTTCT | GTGAGCGCCC | CTGTCCTCCC | GACCTCCATG |
| 2551 | CCCACTCGGG | GGCATGCCTA | GTCCATGTGC | GTAGGGACAG | GCCCTCCCTC |
| 2601 | ACCCATCTAC | CCCCACGGCA | CTAACCCCTG | GCTGCCCTGC | CCAGCCTCGC |
| 2651 | ACCCGCATGG | GGACACAACC | GACTCCGGGG | ACATGCACTC | TCGGGCCCTG |
| 2701 | TGGAGGGACT | GGTGCAGATG | CCCACACACA | CACTCAGCCC | AGACCCGTTC |
| 2751 | AACAAACCCC | GCACTGAGGT | TGGCCGGCCA | CACGGCCACC | ACACACACAC |
| 2801 | GTGCACGCCT | CACACACGGA | GCCTCACCCG | GGCGAACTGC | ACAGCACCCA |
| | | | | | |

FIG. 18C

(SEQ ID NO:22) 2851 GACCAGAGCA AGGTCCTCGC ACACGTGAAC **ACTCCTCGGA** CACAGGCCCC 2901 CACGAGCCCC ACGCGGCACC TCAAGGCCCA CGAGCCTCTC GGCAGCITCT 2951 CCACATGCTG ACCIGCICAG ACAAACCCAG CCCTCCTCTC ACAAGGGTGC 3001 CCCTGCAGCC GCCACACACA CACAGGGGAT CACACACCAC GTCACGTCCC 3051 TGGCCCTGGC CCACTTCCCA GTGCCGCCCT TCCCTGCAGG ACGGATCAGC 3101 CTCGACTGTG CCTTCTAGTT GCCAGCCATC TGTTGTTTGC CCCTCCCCCG 3151 TGCCTTCCTT GACCCTGGAA GGTGCCACTC CCACTGTCCT TTCCTAATAA 3201 AATGAGGAAA TIGCATCGCA TIGICIGAGI AGGTGTCATT CTATTCTGGG 3251 GGGTGGGGTG **GGGCAGGACA GCAAGGGGGA GGATTGGGAA** GACAATAGCA 3301 GGCATGCTGG **GGATGCGGTG GGCTCTATGG** CTTCTGAGGC **GGAAAGAACC** 3351 AGCTGGGGCT CTAGGGGGTA TCCCCACGCG CCCTGTAGCG **GCGCATTAAG** 3401 CGCGGCGGGT GIGGIGGITA CGCGCAGCGT GACCGCTACA CITGCCAGCG 3451 CCCTAGCGCC CGCTCCTTTC GCTTTCTTCC CITCCITICI CGCCACGITC 3501 GCCGGGCCTC TCAAAAAAGG GAAAAAAAGC **ATGCATCTCA** ATTAGTCAGC 3551 AACCATAGTC CCGCCCTAA CICCGCCCAT CCCGCCCCTA ACTCCGCCCA 3601 GTTCCGCCCA TTCTCCGCCC CATGGCTGAC TAATTITTTT TATTTATGCA 3651 GAGGCCGAGG CCGCCTCGGC CTCTGAGCTA TTCCAGAAGT **AGTGAGGAGG** 3701 CITITITGGA GGCCTAGGCT TTTGCAAAAA **GCTTGGACAG** CTCAGGGCTG 3751 CGATTTCGCG CCAAACTIGA CGGCAATCCT AGCGTGAAGG CIGGIAGGAT 3801 TITATCCCCG GGTTCGACCA CTGCCATCAT TIGAACIGCA TCGTCGCCGT 3851 GTCCCAAAAT ATGGGGATTG GCAAGAACGG AGACCTACCC TGGCCTCCGC 3901 TCAGGAACGA GITCAAGIAC TTCCAAAGAA TGACCACAAC CICITCAGIG 3951 GAAGGTAAAC AGAATCTGGT GATTATGGGT AGGAAAACCT GGITCICCAT 4001 TCCTGAGAAG AATCGACCIT TAAAGGACAG **AATTAATATA** GTTCTCAGTA 4051 GAGAACTCAA AGAACCACCA CGAGGAGCTC ATTTTCTTGC CAAAAGTTTG 4101 GATGATGCCT TAAGACTTAT TGAACAACCG GAATTGGCAA GTAAAGTAGA 4151 CATGGTTTGG ATAGTCGGAG GCAGTTCTGT TTACCAGGAA **GCCATGAATC** 4201 AACCAGGCCA CCTTAGACTC TTTGTGACAA **GGATCATGCA GGAATTTGAA 4251 AGTGACACGT** TITITCCCAGA AATTGATTTG **GGGAAATATA** AACTTCTCCC 4301 AGAATACCCA GGCGTCCTCT CIGAGGICCA **GGAGGAAAAA GGCATCAAGT**

FIG. 18D

| 4351 | ATAAGTTTG! | A AGTCTACGAO | SEQ ID NO:22 | | A TGCTTTCAAG |
|------|--------------------|--------------|--------------|-------------|--------------|
| 4401 | TTCTCTGCT | CCCTCCTAA | GCTATGCAT | r titataaga | CATGGGACTT |
| 4451 | TTGCTGGCTT | TAGATCTCTT | TGTGAAGGA | CCTTACTTC1 | GTGGTGTGAC |
| 4501 | ATAATTGGAC | : AAACTACCTA | CAGAGATTTA | AAGCTCTAAG | GTAAATATAA |
| 4551 | AATTTTTAAG | TGTATAATGT | GTTAAACTAC | TGATTCTAAT | TGTTTGTGTA |
| 4601 | TTTTAGATTC | CAACCTATGG | AACTGATGAA | TGGGAGCAGT | GGTGGAATGC |
| 4651 | CTTTAATGAG | GAAAACCTGT | TTTGCTCAGA | AGAAATGCCA | TCTAGTGATG |
| 4701 | ATGAGGCTAC | TGCTGACTCT | CAACATTCTA | CTCCTCCAAA | AAAGAAGAGA |
| 4751 | AAGGTAGAAG | ACCCCAAGGA | CTTTCCTTCA | GAATTGCTAA | GTTTTTTGAG |
| 4801 | TCATGCTGTG | TTTAGTAATA | GAACTCTTGC | TTGCTTTGCT | ATTTACACCA |
| 4851 | CAAAGGAAAA | AGCTGCACTG | CTATACAAGA | aaattatgga | AAAATATTCT |
| 4901 | GTAACCTTTA | TAAGTAGGCA | TAACAGTTAT | AATCATAACA | TACTGTTTTT |
| 4951 | TCTTACTCCA | CACAGGCATA | GAGTGTCTGC | TATTAATAAC | TATGCTCAAA |
| 5001 | AATTGTGTAC | CTTTAGCTTT | TTAATTTGTA | AAGGGGTTAA | TAAGGAATAT |
| 5051 | TTGATGTATA | GTGCCTTGAC | TAGAGATCAT | AATCAGCCAT | ACCACATTTG |
| 5101 | TAGAGGTTTT | ACTTGCTTTA | AAAAACCTCC | CACACCTCCC | CCTGAACCTG |
| 5151 | АААСАТААА А | TGAATGCAAT | TGTTGTTGTT | AACTTGTTTA | TTGCAGCTTA |
| 5201 | TAATGGTTAC | AAATAAAGCA | ATAGCATCAC | AAATTTCACA | AATAAAGCAT |
| 5251 | TTTTTTCACT | GCATTCTAGT | TGTGGTTTGT | CCAAACTCAT | CAATGTATCT |
| 5301 | TATCATGTCT | GGATCGGCTG | GATGATCCTC | CAGCGCGGGG | ATCTCATGCT |
| 5351 | GGAGTTCTTC | GCCCACCCCA | ACTTGTTTAT | TGCAGCTTAT | AATGGTTACA |
| 5401 | AATAAAGCAA | TAGCATCACA | AATTTCACAA | ATAAAGCATT | TTTTTCACTG |
| 5451 | CATTCTAGTT | GTGGTTTGTC | CAAACTCATC | AATGTATCTT | ATCATGTCTG |
| 5501 | TATACCGTCG | ACCTCTAGCT | AGAGCTTGGC | GTAATCATGG | TCATAGCTGT |
| 5551 | TTCCTGTGTG | AAATTGTTAT | CCGCTCACAA | TTCCACACAA | CATACGAGCC |
| 5601 | GGAAGCATAA | AGTGTAAAGC | CTGGGGTGCC | TAATGAGTGA | GCTAACTCAC |
| 5651 | ATTAATTGCG | TTGCGCTCAC | TGCCCGCTTT | CCAGTCGGGA | AACCTGTCGT |
| 5701 | GCCAGCTGCA | TTAATGAATC | GGCCAACGCG | CGGGGAGAGG | CGGTTTGCGT |
| 5751 | ATTGGGCGCT | CTTCCGCTTC | CTCGCTCACT | GACTCGCTGC | GCTCGGTCGT |
| 5801 | TCGGCTGCGG | CGAGCGGTAT | CAGCTCACTC | AAAGGCGGTA | ATACGGTTAT |

FIG. 18E

| | | (SEQ I | D NO:22) | | |
|------|------------|------------|------------|------------|------------|
| 5851 | CCACAGAATC | AGGGGATAAC | GCAGGAAAGA | ACATGIGAGC | AAAAGGCCAG |
| 5901 | CAAAAGGCCA | GGAACCGTAA | AAAGGCCGCG | TIGCIGGCGT | TTTTCCATAG |
| 5951 | ecrececce | CCTGACGAGC | ATCACAAAAA | TCGACGCTCA | AGTCAGAGGT |
| 6001 | GGCGAAACCC | GACAGGACTA | TAAAGATACC | AGGCGTTTCC | CCCTGGAAGC |
| 6051 | TCCCTCGTGC | GCTCTCCTGT | TCCGACCCTG | CCGCTTACCG | GATACCIGIC |
| 6101 | CGCCTTTCTC | CCTTCGGGAA | GCGTGGCGCT | TTCTCAATGC | TCACGCTGTA |
| 6151 | GGTATCTCAG | TICGGIGTAG | GTCGTTCGCT | CCAAGCTGGG | CTGTGTGCAC |
| 6201 | GAACCCCCCG | TTCAGCCCGA | CCGCTGCGCC | TTATCCGGTA | ACTATCGTCT |
| 6251 | TGAGTCCAAC | CCGGTAAGAC | ACGACTTATC | GCCACTGGCA | GCAGCCACTG |
| 6301 | GTAACAGGAT | TAGCAGAGCG | AGGTATGTAG | GCGGTGCTAC | AGAGTICITG |
| 6351 | AAGTGGTGGC | CTAACTACGG | CTACACTAGA | AGGACAGTAT | TIGGTATCIG |
| 6401 | CGCTCTGCTG | AAGCCAGTTA | CCTTCGGAAA | AAGAGTTGGT | AGCTCTTGAT |
| 6451 | CCGGCAAACA | AACCACCGCT | GGTAGCGGTG | GITTITITGT | TTGCAAGCAG |
| 6501 | CAGATTACGC | GCAGAAAAAA | AGGATCTCAA | GAAGATCCTT | TGATCTTTTC |
| 6551 | TACGGGGTCI | GACGCTCAGT | GGAACGAAAA | CTCACGITAA | GGGATTTTGG |
| 6601 | TCATGAGATT | ATCAAAAAGG | ATCTTCACCT | AGATCCITIT | AAATTAAAA |
| 6651 | TGAAGTTITA | AATCAATCTA | AAGTATATAT | GAGTAAACIT | GGTCTGACAG |
| 6701 | TTACCAATGC | TTAATCAGTG | AGGCACCTAT | CTCAGCGATC | TGTCTATTTC |
| 6751 | GITCATCCAT | AGTTGCCTGA | CTCCCCGTCG | TGTAGATAAC | TACGATACGG |
| 6801 | GAGGGCTTAC | CATCTGGCCC | CAGTGCTGCA | ATGATACCGC | GAGACCCACG |
| 6851 | CTCACCGGCT | CCAGATTTAT | CAGCAATAAA | CCAGCCAGCC | GGAAGGGCCG |
| 6901 | AGCGCAGAAG | TGGTCCTGCA | ACTITATECG | CCTCCATCCA | GTCTATTAAT |
| 6951 | TGTTGCCGGG | AAGCTAGAGT | AAGTAGTTCG | CCAGTTAATA | GTTTGCGCAA |
| 7001 | CGTTGTTGCC | ATTGCTACAG | GCATCGTGGT | GTCACGCTCG | TCGTTTGGTA |
| 7051 | TGGCTTCATT | CAGCTCCGGT | TCCCAACGAT | CAAGGCGAGT | TACATGATCC |
| 7101 | CCCATGTTGT | GCAAAAAAGC | GGTTAGCTCC | TTCGGTCCTC | CGATCGTTGT |
| 7151 | CAGAAGTAAG | TIGGCCGCAG | TGTTATCACT | CATGGTTATG | GCAGCACTGC |
| 7201 | ATAATTCTCT | TACTGTCATG | CCATCCGTAA | GATGCTTTTC | TGTGACTGGT |
| 7251 | GAGTACTCAA | CCAAGTCATT | CTGAGAATAG | TGTATGCGGC | GACCGAGTTG |
| 7301 | CTCTTGCCCG | GCGTCAATAC | GGGATAATAC | CGCGCCACAT | AGCAGAACTT |

FIG. 18F

(SEQ ID NO:22)

| | | (SEQ ID | NO:22) | | |
|------|------------|-------------|-------------|------------|------------|
| 7351 | TAAAAGTGCT | CATCATTGGA | AAACGTICTT | CGGGGCGAAA | ACTCTCAAGG |
| 7401 | ATCTTACCGC | TGTTGAGATC | CAGTTCGATG | TAACCCACTC | GTGCACCCAA |
| 7451 | CTGATCTTCA | GCATCTTTTA | CTTTCACCAG | CGTTTCTGGG | TGAGCAAAAA |
| 7501 | CAGGAAGGCA | AAATGCCGCA | AAAAAGGGAA | TAAGGGCGAC | ACGGAAATGT |
| 7551 | TGAATACTCA | TACTCTTCCT | TITITCAATAT | TATTGAAGCA | TTTATCAGGG |
| 7601 | TTATTGTCTC | ATGAGCGGAT | ACATATITGA | ATGTATTTAG | AAAAATAAAC |
| 7651 | AAATAGGGGT | TCCGCGCACA | TTTCCCCGAA | AAGTGCCACC | TGACGTCGAC |
| 7701 | GGATCGGGAG | ATCIGCTAGG | TGACCTGAGG | CGCGCCGGCT | TCGAATAGCC |
| 7751 | AGAGTAACCT | TTTTTTTTAA | TTTTATTTTA | TTTTATTTT | GAGATGGAGT |
| 7801 | TTGGCGCCGA | TCTCCCGATC | CCCTATGGTC | GACTOTCAGT | ACAATCTGCT |
| 7851 | CTGATGCCGC | ATAGTTAAGC | CAGTATCTGC | TOCOTGOTTG | TGTGTTGGAG |
| 7901 | GTCGCTGAGT | AGTGCGCGAG | CAAAATTTAA | GCTACAACAA | GGCAAGGCTT |
| 7951 | GACCGACAAT | TGCATGAAGA | ATCTGCTTAG | GGTTAGGCGT | TITGCGCTGC |
| 8001 | TTCGCGATGT | ACGGGCCAGA | TATACGCGTT | GACATTGATT | ATTGACTAGT |
| 8051 | TATTAATAGT | AATCAATTAC | GGGGTCATTA | GTTCATAGCC | CATATATGGA |
| 8101 | GTTCCGCGTT | ACATAACTTA | CGGTAAATGG | CCCGCCTGGC | TGACCGCCCA |
| 8151 | ACGACCCCCG | CCCATTGACG | TCAATAATGA | CGTATGTTCC | CATAGTAACG |
| 8201 | CCAATAGGGA | CTTTCCATTG | ACGTCAATGG | GTGGACTATT | TACGGTAAAC |
| 8251 | TGCCCACTTG | GCAGTACATC | AAGTGTATCA | TATGCCAAGT | ACGCCCCTA |
| 8301 | TTGACGTCAA | TGACGGTAAA | TGGCCCGCCT | GGCATTATGC | CCAGTACATG |
| 8351 | ACCITATEGE | ACTITICCTAC | TIGGCAGTAC | ATCTACGTAT | TAGTCATCGC |
| 8401 | TATTACCATG | GTGATGCGGT | TITEGCAGTA | CATCAATGGG | CGTGGATAGC |
| 8451 | GGTTTGACTC | ACGGGGATTT | CCAAGTCTCC | ACCCCATTGA | CGTCAATGGG |
| 8501 | AGITTGITIT | GGCACCAAAA | TCAACGGGAC | TITCCAAAAT | GTCGTAACAA |
| 8551 | CTCCGCCCCA | TTGACGCAAA | TEGECGETAG | GCGTGTACGG | TGGGAGGTCT |
| 8601 | ATATAAGCAG | AGCTCTCTGG | CTAACTAGAG | AACCCACTGC | TTACTGGCTT |
| 8651 | ATCGAAATTA | ATACGACTCA | CTATAGGGAG | ACCCAAGCTT | |
| | | | | | |

FIG. 19A Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

| pD17-hG1b | 60 | 120 | 180 | 240 | 300 | 360 | 420 | 480 | 540 | 600 |
|-----------|--------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|
| | GGTCAATCGA | CCTGGCACCC | GGACTACTTC | GCACACCTIC | CGTGCCCTCC | CAACACCAAG | TGGRAGCCAG | GCAGCAAGGC | TCAGGGAGAG | CTAACCCAGG |
| | CCAGTTAGCT | GGACCGTGGG | CCTGATGAAG | CGTGTGGAAG | GCACGGGAGG | GITGIGGIIC | ACCTTCGGTC | CGTCGTTCCG | AGTCCCTCTC | GAITGGGGICC |
| g G | 50 CTAGATAACC GATCTAITGG | 110 CGGTCTTCCC GCCAGAAGGG | 170 GCCTGGTCAA CGGACCAGTT | 230 CCAGCGGCGT GGTCGCCGCA | 290 GCGTGGTCAC CGCACCAGTG | 350 ACAAGCCCAG TOTTCGGGTC | 410 GGGTGTCTGC CCCACAGACG | 470 CCAGTCCAGG GGTCAGGTCC | 530 CCACTCATGC GGTGAGTACG | 590 CTAGGTGCCC GATCCACGGG |
| | 40 | 100 | 160 | 220 | 280 | 340 | 400 | 460 | 520 | 580 |
| | TCTCGAGTCT | AAGGGCCAT | GCCCTGGGCT | GGCGCCCTGA | TCCCTCAGCA | AACGTGAATC | CAGGGAGGGA | CTATGCAGCC | TCTGCCCGCC | CAGGCACAGO |
| | AGAGCTCAGA | TTCCCGGGTA | CGGGACCCGA | CCGCGGGACT | AGGGAGTCGT | TTGCACTTAG | GTCCCTCCCT | GATACGTCGG | AGACGGGCGG | GICCGIGICC |
| | 30 | 90 | 150 | 210 | 270 | 330 | 390 | 450 | 510 | 570 |
| | TCTCCTTAGG | TGCTAGCACC | GGGCACAGCG | GTGGAACTCA | AGGACTCTAC | CTACATCTGC | GAGGCCAGCA | CGCATCCCGG | CCCGGAGGCC | AGGCICIGGG |
| | AGAGGAATCC | ACGATCGTGG | CCCGTGTCGC | CACCTTGAGT | TCCTGAGATG | GATGTAGACG | CTCCGGTCGT | GCGTAGGGCC | GGGCTCCGG | TCCGAGACCC |
| | 20 | 80 | 140 | 200 | 260 | 320 | 380 | 440 | 500 | 560 |
| | TAAATTGATA | TGCGGCCG CT | GCACCTCTGG | TGACGGTGTC | TACAGTCCTC | GCACCCAGAC | AAGTIGGIGA | CCTGCCTGGA | TGCCTCTTCA | CITITICCCC |
| | ATTTAACTAT | ACGCCGGCGA | CGTGGAGACC | ACTGCCACAG | ATGTCAGGAG | CGTGGGTCTG | TICAACCACI | GGACGGACCT | ACGGAGAAGT | GRARARGGGG |
| | 10 | 70 | 130 | 190 | 250 | 310 | 370 | 430 | 490 | 550 |
| | GGTACCAATT | TTGGAATTCT | TCCTCCAAGA | CCCGAACGGG | CCGGCTGICC | AGCAGCITGG | GTGGACAAGA | GCTCAGCGCT | AGGCCCGTC | GGTCTTCTGG |
| | CCATGGTTAA | AACCTTAAGA | AGGAGGTTCT | GGGCTTGGCC | GGCCGACAGG | TCGTCGAACC | CACCTGTTCT | CGAGTCGCGA | TCCGGGGCAG | CCAGAAGACC |
| | | | | | | | | | | |

32/53

FIG. 19B Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

| 7-hG1b 660 rccgggagga aggcccrccr | 720 AGCTCGGACA TCGAGCCTGT | 780 CCAAATCTTG GGTTTAGAAC | 840 CGCCCTCCAG GCGGAGGTC | 900 cagccgggrg grcggcccac | 960 CCGTCAGTCT GGCAGTCAGA | 1020 GAGGTCACAT CTCCAGTGTA | 1080 TACGTGGACG ATGCACCTGC | 1140 AGCACGTACC TCGTGCATGG 320 | 318 1200 GAGTACAAGT CTCATGTTCA |
|--|--------------------------------------|---------------------------------|-------------------------------------|---------------------------------|---------------------------------|--------------------------------------|----------------------------------|---|--------------------------------------|
| pD17-hG1b 650 aagagccata rccggg rrcrcggrar aggccc | 710 CCACTCCTC AC GGTGAGGGAG TC | 770 TCTGCAGAGC CO | 830 GCCCAGGCCT C CGGGTCCGGA G | | 235 950 CCTGGGGGGA C | 1010 CCGGACCCCT C GGCCTGGGGA C | 1070 GTTCAACTGG | 1130 GCAGTACAAC CGTCATGTTG | 1190 GANTGGCAAG CTTACCGTTC |
| 640 CAGACCTGCC 7 | 700 GCCAAACTCT CGGTTTGAGA | 760 CAATCTTCTC GTTAGAAGAG | 820 AGGTAAGCCA TCCATTCGGT | 880 CTGCATCCAG GACGTAGGTC | 940 CACCTGAACT GTGGACTTGA | 1000 TCATGATCTC AGTACTAGAG | 1060 CTGAGGTCAA GACTCCAGTT | 1120 CGCGGGAGGA GCGCCCTCCT | 1180 AGGACTGGCT TCCTGACCGA |
| 630 GTGCTGGGCT C | 690 CACCCCAAAG GTGGGGTTTC | 750 CAGTAACTCC GTCATTGAGG | 810 CACCGTGCCC GTGGCACGGG | 870 CTAGAGTAGC GATCTCATCG | 930 TCTTCCTCAG AGAAGGAGTC | 990 AAGGACACCC TTCCTGTGGG | 1050 CACGAAGACC GTGCTTCTGG | 1110 AAGACAAAGC TTCTGTTTCG | 1170 GTCCTGCACC CAGGACGTGG |
| 620 AAAGGGGCAG (TITECCCGGTC) | 680 GACCTAAGCC CTGGATTCGG | 740 TCCCAGATTC AGGGTCTAAG | 800 CACACATGCC GTGTGTACGG | 860 GACAGGTGCC CTGTCCACGG | 920 CACCTCCATC GTGGAGGTAG | 980 CCCAAAACCC GGGTTTTGGG | 1040 GGACGTGAGC CCTGCACTCG | 1100 GCATAATGCC CGTATTACGG | 1160 CGTCCTCACC GCAGGAGTGG |
| 610 CCCTGCACAC A | 670 CCCTGCCCCT GGGACGGGGA | 730 CCTTCTCCC GGAAGAGAGG | 790 TGACAAAACT ACTGTTTTGA | 850 CTCAAGGCGG GAGTTCCGCC | 910 CTGACACGTC GACTGTGCAG | 970 TCCTCTTCCC AGGAGAAGGG | 1030 GCGTGGTGGT CGCACCACCA | 1090 GCGTGGAGGT CGCACCTCCA | 1150 GTGTGGTCAG CACACCAGTC |

33/53

FIG. 19C Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

| pul/-ngid 50 cc aaagccaaag gg tytcggyyc | 1320 ACCCTCTGCC TGGGAGACGG | 1380 ACCACAGGTG TGGTGTCCAC | 1440 GACCTGCCTG CTGGACGGAC | 1500 GCAGCCGGAG CGTCGGCCTC | 1560 CCTCTACAGC GGAGATGTCG | 1620 CTCCGTGATG GAGGCACTAC | 1680 GGGTAAATGA CCCATTTACT | 1740 GATGCTTGGC CTACGAACCG | 1800 CCAGCGCTGC GGTCGCGACG |
|--|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|
| pU1 1250 AACCATCTCC TTGGTAGAGG | 1310 GGCTCGGCCC CCGAGCCGGG | 1370 AGCCCCGAGA TCGGGGCTCT | 1430 AGGTCAGCCT TCCAGTCGGA | 1490 AGAGCAATGG TCTCGTTACC | 1550 GCTCCTTCTT CGAGGAAGAA | 1610 TCTTCTCATG AGAAGAGTAC | 1670 CCCTGTCTCC GGGACAGAGG | 1730 GTCGCACGAG CAGCGTGCTC | 1790 AATAAAGCAC TTATTTCGTG |
| 31 1240 | 1300 | 1360 | 1420 | 1480 | 1540 | 1600 | 1660 | 1720 | 1780 |
| CCATCGAGAA | Gacagaggc | CCTACAGGGC | ACCAAGAACC | GTGGAGTGGG | GACTCCGACG | CAGGGGAACG | AAGAGCCTCT | ggctctcgcg | CCAGCATGGA |
| GGTAGCTCTT | Ctgtctccgg | GGATGTCCCG | TGGTTCTTGG | CACCTCACCC | CTGAGGCTGC | GTCCCCTTGC | TTCTCGGAGA | ccgagagcgc | GGTCGTACCT |
| 1230331 | 1290 | 1350 | 1410 | 1470 | 1530 | 1590 | 1650 | 1710 | 1770 |
| CTCCCAGCCC CC | GGGCCACATG | AACCTCTGTC | GGATGAGCTG | CGACATCGCC | TCCCGTGCTG | CAGGTGGCAG | CTACACGCAG | ccecrcccc | TCCCGGGCGC |
| GAGGGTCGGG GG | CCCGGTGTAC | TTGGAGACAG | CCTACTCGAC | GCTGTAGCGG | AGGGCACGAC | GTCCACCGTC | GATGTGCGTC | gccgAgcccc | AGGGCCCGCG |
| 1220 | 1280 | 1340 | 1400 | 1460 | 1520 | 1580 | 1640 | 1700 | 1760 |
| CAACAAAGCC | TGGGGTGCGA | CCGCTGTACC | CCCCATCCCG | TCTATCCCAG | AGACCACGCC | TGGACAAGAG | TGCACAACCA | CGGCAAGCCC | TGTACATACT |
| GTYGTTTCGG | ACCCCACGCT | GGCGACATGG | GGGGTAGGGC | AGATAGGGTC | TCTGGTGCGG | ACCTGTTCTC | ACGTGTTGGT | GCCGTTCGGG | ACATGTATGA |
| 322 1210 | 1270 | 1330 | 1390 | 1450 | 1510 | 1570 | 1630 | 1690 | 1750 |
| GCAAGGICIC | GTGGGACCCG | CTGAGAGTGA | TACACCCTGC | GTCAAAGGCT | AACAACTACA | AAGCTCACCG | CATGAGGCTC | GTGCGACGGC | ACGTACCCC |
| CGTICCAGAG | CACCCTGGGC | GACTCTCACT | ATGTGGGACG | CAGTTTCCGA | TYGTTGATGT | TYCGAGTGGC | GTACTCCGAG | CACGCTGCCG | TGCATGGGGG |

34/53

FIG. 19D Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

| pD17-hG1b so 1860 | CTGAGGCCTG GACTCCGGAC | 1920 GCTGTGCAGG CGACACGTCC | 1980 GGTGGGGAT CCACCCCTA | 2040 GGAAGCCCTA CCTTCGGGAT | 2100 TGTTCTGTGA ACAAGACACT | 2160 GCGGTGGGCT CGCCACCCGA | 2220 CACGCGCCCT GTGCGCGGA | 2280 GCTACACITG CGAIGIGAAC | 2340 ACGITCGCCG TGCAAGCGGC | 2400 AGIGCITIAC TCACGABAIG |
|---------------------------------------|--------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|
| pD1 1850 | CAGGCCGAGT | 1910 ACTGGCCCAG TGACCGGGTC | 1970 CCCTCGGCAG GGGAGCCGTC | 2030 CIGGGCCACG GACCCGGIGC | 2090 GAGACTGICC CTCTGACAGG | 2150 TGCTGGGGAT ACGACCCCTA | 2210 GGGGTATCCC CCCCATAGGG | 2270 CAGCGTGACC GTCGCACTGG | 2330 CITICICGCC GAAAGAGCGG | 2390 GITCCGAITT CAAGGCTAAA |
| 1840 | TTCCACGGGT | 1900 CTGTCCCCAC GACAGGGGTG | 1960 CCAGGGGCTG GGTCCCCGAC | 2020 CTGCCCTGGG GACGGGACCC | 2080 GCCTCTGTAG CGGAGACATC | 2140 CTCGGGGGCA GAGCCCCCT | 2200 GGGCTCTAG CCCCGAGATC | 2260 TGGITACGCG ACCAATGCGC | 2320 TCTTCCCTTC AGAAGGGAAG | 2380 TCCCTTTAGG AGGGAAATCC |
| CF8. | TGATGGTTCT | 1890 GCGGGTCCCA CGCCCAGGGT | 1950 TGGGGCTCAG ACCCCGAGTC | 2010 CCAGCAGCAC GGTCGTCGTG | 2070 CACAGCCCCT GTGTCGGGGA | 2130 TCCATGCCCA AĠGTACGGGT | 2190 AGAACCAGCT TCTTGGTCGA | 2250 GCGGGTGTGG CGCCCACACC | 2310 CCTTTCGCTT GGRARGCGRA | 2370 AATCGGGGCA TTAGCCCCGT |
| C C C C C C C C C C C C C C C C C C C | TGCGAGACTG ACGCTCTGAC | 1880 GGGAGGCAGA CCCTCCGTCT | 1940 CCCCTAGGG GGGGGATCCC | 2000 GGCCCTCCCT CCGGGAGGGA | 2060 GGGACAGACA CCCTGTCTGT | 2120 CCTCCCGACC GGAGGGCTGG | 2180 TGAGGCGGAA ACTCCGCCTT | 2240 ATTAAGCGCG TAATTCGCGC | 2300 AGCGCCGCT TCGCGGGCGA | 2360 TCAAGCTCTA AGTTCGAGAT |
| , , | CCTGGGGCCCC | 1870 AGTGGCATGA TCACCGTACT | 1930 TGTGCCTGGG ACACGGACCC | 1990 TTGCCAGCGT AACGGTCGCA | 2050 GGAGCCCCTG CCTCGGGGAC | 2110 GCGCCCTGT CGCGGGGACA | 2170 CTATGGCTTC GATACCGAAG | 2230 GTAGCGGCGC CATCGCCGCG | 2290 CCAGGGGCCT GGTCGCGGGA | 2350 GCTTTCCCG CGAAAGGGGC |
| | | | | | | | : | | | |

35/53

FIG. 19E Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

| pD17-hG1b | 2460 | 2520 | 2580 | 2640 | 2700 | 2760 | 2820 | 2880 | 2940 | 3000 |
|-----------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|-----------------------------------|----------------------------------|----------------------------------|----------------------------------|
| | CCATCGCCCT | GGACTCTTGT | TAAGGGATTT | AACGCGAATT | CAGGCAGGCA | CTAACTCCGC | TGACTAATTT | AAGTAGTGAG | GCTGCGATT | CCCGCTGCCA |
| | GGTAGCGGGA | CCTGAGAACA | ATTCCCTAAA | TTGCGCTTAA | GTCCGTCCGT | GATTGAGGCG | ACTGATTAAA | TTCATCACTC | CGACGCTAAA | GGGCGACGGT |
| PD1 | 2450 | 2510 | 2570 | 2630 | 2690 | 2750 | 2810 | 2870 | 2930 | 2990 |
| | ACCINGIGGG | CITIAAIAGI | TYTYGATTTA | ACAAAAATT | CCAGGCTCCC | AGTCCCGCC | GCCCCATGGC | GCTATTCCAG | ACAGCTCAGG | GGATTITATC |
| | TGCATCACCC | GAAAIIAICA | AAAACTAAAT | TGITTITAAA | GGTCCGAGGG | TCAGGGCGGG | CGGGGTACCG | CGATAAGGTC | TGTCGAGTCC | CCIABABIAG |
| | 2440 GTGATGGTTC 2 | 2500 AGTCCACGIT TCAGGIGCAA | 2560 CGGTCTATTC GCCAGATAAG | 2620 AGCTGATTIA TCGACTAAAT | 2680 TUGAANGTCC ACCITTCAGG | 2740 CAGCAACCAT GTCGTTGGTA | 2800 CCCATTCTCC GGGTAAGAGG | 2860 CGGCCTCTGA GCCGGAGACT | 2920 AAAAGCTTGG TTTTCGAACC | 2980 AAGGCTGGTA TTCCGACCAT |
| | 2430 CTTGATTAGG GAACTAATCC | 2490 TTGACGITGG | 2550 AACCCIAICI TIGGGAIAGA | 2610 TTAAAAATG AATITITIAC | 2670 AGITAGGGIG TCAAICCCAC | 2730 CTCAATTAGT GAGTTAATCA | 2790 CCCAGITICCG GGGICAAGGC | 2850 GAGGCGGCT CTCCGGCGGA | 2910 GGCTTTTGCA CCGARAACGT | 2970 TCCTAGCGTG AGGATCGCAC |
| | 2420 | 2480 | 2540 | 2600 | 2660 | 2720 | 2780 | 2840 | 2900 | 2960 |
| | CCCCRARARA (| TTTTCGCCCT | AACAACACTC | GGCCTATTGG | AATGTGTGTC | AAGCATGCAT | CCTAACTCCG | TGCAGAGGCC | TGGAGGCCTA | ITGACGGCAA |
| | GGGGTTTTTT | AAAAGCGGGA | TTGTTGTGAG | CCGGATAACC | TTACACACAG | TTCGTACGTA | GGATTGAGGC | ACGTCTCCGG | ACCTCCGGAT | AACTGCCGIT |
| | 2410 | 2470 | 2530 | 2590 | 2650 | 2710 | 2770 | 2830 | 2890 | 2950 |
| | GGCACCTCGA C | GATAGACGGT | TCCAAACTGG | TGGGGATTTC | AATICIGIGG | GANGTATGCA | CCATCCCGC | TITITATITA | GAGGCITITI | CGCGCCAAAC |
| | CCGTGGAGCT (| CTATCTGCCA | AGGTTTGACC | ACCCCTAAAG | TIAAGACACC | CPTCATACGT | GGTAGGGCGG | AAAAAAAATAAAT | CICCGAAAAA | GCGCGGTTTG |

36/53

FIG. 19F Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

| pD17-hG1b | 3060 ATTGGCAAGA TAACCGTTCT | 3120 AGAATGACCA TCTTACTGGT | 3180 ACCIGGITCI TGGACCAAGA | 3240 AGTAGAGAAC TCATCTTG | 3300 GCCTTAAGAC CGGAATTCTO | 3360 GGAGGCAGIT CCTCCGICAA | 3420 ACAAGGATCA TGTTCCTAGT | 3480 TATAAACTTC ATATTTGAAG | 3540 AAGTATAAGT TTCATATTCA | 3600 GCTCCCCTCC |
|-----------|----------------------------------|----------------------------------|----------------------------------|--------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|--------------------|
| O0 | 3050 | 3110 | 3170 | 3230 | 3290 | 3350 | 3410 | 3470 | 3530 | 3590 |
| | ANATATGGGG | GTACTTCCAA | GGGTAGGAAA | TATAGITCTC | TTTGGATGAT | TTGGATAGTC | ACTCTTIGIG | TITGGGAAA | AAAAGGCATC | Caagitcici |
| | TTTATACCCC | CATGAAGGTT | CCCATCCTTT | ATATCAAGAG | AAACCTACTA | AACCTATCAG | TGAGAAACAC | AAACCCCIIT | TITTCCGTAG | Gitcaagaga |
| | 3040 | 3100 | 3160 | 3220 | 3280 | 3340 | 3400 | 3460 | 3520 | 3580 |
| | CCGTGTCCCA | ACGAGIICAA | TGGTGATTAT | ACAGAATTAA | TTGCCAAAAG | TAGACATGGT | GCCACCTTAG | CAGAAATTGA | TCCAGGAGGA | AAGATGCTT |
| | GGCACAGGGT | TGCICAAGII | ACCACTAATA | TGTCTTAATT | AACGGTTTTC | ATCTGTACCA | CGGTGGAATC | GTCTTTAACT | AGGTCCTCCT | TTCTACGAAA |
| | 3030 | 3090 | 3150 | 3210 | 3270 | 3330 | 3390 | 3450 | 3510 | 3570 |
| | TGCATCGTCG | CCGCTCAGGA | AAACAGAATC | CCTTTBAAGG | GCTCATTTTC | GCAAGTAAAG | AATCAACCAG | ACCITITIC | CTCTCTGAGG | GACTAACAGG |
| | ACGTAGCAGC | GGCGAGTCCT | TTTGTCTTAG | GGAAATTTCC | CGAGTAAAAG | CGTTCATTTC | TTAGTTGGTC | TGCAAAAAGG | GAGAGACTCC | CTGATTGTCC |
| | 3020 | 3080 | 3140 | 3200 | 3260 | 3320 | 3380 | 3440 | 3500 | 3560 |
| | ACCATTGAAC | ACCCTGGCCT | AGTGGAAGGT | GAAGAATCGA | ACCACGAGGA | ACCGGAATTG | GGAAGCCATG | TGAAAGTGAC | CCCAGGCGTC | CGAGAAGAAA |
| | TGGTAACTTG | TGGGACCGGA | TCACCTTCCA | CTTCTTAGCT | TGGTGCTCCT | TGGCCTTAAC | CCTTCGGTAC | ACTITCACTG | GGGTCCGCAG | GCTCTTCTTT |
| | 3010 | 3070 | 3130 | 3190 | 3250 | 3310 | 3370 | 3430 | 3490 | 3550 |
| | TCATGGTTCG | ACGGAGACCT | CAACCICITC | CCATTCCTGA | TCAAAGAACC | TTATTGAACA | CIGITIACCA | TGCAGGAATT | TCCCAGAATA | TYGAAGICTA |
| | AGTACCAAGC | TGCCTCTGGA | GITGGAGAAG | GGTAAGGACT | AGTTTCTTGG | AATAACTIGT | GACAAAIGGI | ACGTCCTTAA | AGGGTCTTAT | AACTICAGAT |
| | | | | | | | | | | |

37/53

FIG. 19G Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

| 3720 | 3780 | 3840 | 3900 | 3960 | 4020 | 4080 | 4140 | 4200 |
|------------|--|--|--|--|--|--|---|---|
| TTTAAAGCTC | TAATTGTTTG | ATGCCTTTAA | CIACTGCTGA | AGGACTITCC | TIGCIIGCII | TGGAAAATA | TITITCITAC | GTACCTTTAG |
| AAATTTCGAG | ATTAACAAAC | TACGGAAATT | GATGACGACT | TCCTGAAAGG | AACGAACGAA | ACCTTTTTAT | AAAAAGAATG | CATGGAAATC |
| 3710 | 3770 | 3830 | 3890 | 3950 | 4010 | 4070 | 4130 | 4190 |
| CCTACAGAGA | CTACTGATTC | CAGTGGTGGA | GATGATGAGG | GAAGACCCCA | PATAGRACIC | AAGAAAATTA | AACATACTGT | CAAAAATTGT |
| GGATGTCTCT | GATGACTAAG | GTCACCACCT | CTACTACTCC | CITCIGGGGI | TTRICITGAG | TTCTITTAAT | TTGTATGACA | GITTITAACA |
| 3700 | 3760 | 3820 | 3880 | 3940 | 4000 | 4060 | 4120 | 4180 |
| ggrcaaacta | Atgtgttaaa | TGAATGGGAG | GCCATCTAGT | GAGAAAGGIA | TGTGTTTAGT | ACTGCTATAC | TTATAATCAT | TAACTATGCT |
| cctgrttgat | Tacacaattt | ACTTACCCTC | CGGTAGATCA | CTCTTTCCAI | ACACABATCA | TGACGATATG | AATATTAGTA | ATTGATACGA |
| 3690 | 3750 | 3810 | 3870 | 3930 | 3990 | 4050 | 4110 | 4170 |
| TCACATARIT | TRAGIGIATA | ATGGAACTGA | CAGAAGAAAT | CAAAAAAAA | TGAGTCATGC | Araractec | GGCATAACAG | CTGCTATTAA |
| ACTOTATTAA | ATICACATAI | TACCTTGACT | GTCTTTTA | GIIIYIICII | ACTCAGTACG | Titicgace | CCGTATTGTC | GACGATAATT |
| 3680 | 3740 | 3800 | 3860 | 3920 | 3980 | 4040 | 4100 | 4160 |
| TTCTGTGGTG | ATAAAATITT | ATTCCAACCT | CTGTTTTGCT | TCTACTCCTC | CTANGTIFFT | ACCACAAAGG | TTTATAAGTA | CATAGAGTGT |
| AAGACACCAC | TATTITAAA | TAAGGTTGGA | GACAAAAGGA | AGATGAGGAG | GATTCAAAAA | TGGTGTTTCC | AAATATTCAT | GTATCTCACA |
| 3670 | 3730 | 3790 | 3850 | 3910 | 3970 | 4030 | 4090 | 4150 |
| GGAACCTTAC | TAAGGTAAAT | TGTATTTFAG | TGAGGAAAAC | CICTCAACAT | TICAGAATIG | TGCTATTTAC | TTCTGTAACC | TCCACACAGG |
| CCTTGGAATG | ATTCCATTTA | ACATAAAATC | ACTCCTTTTG | GAGAGTIGIA | AAGICTTAAC | ACGATAAATG | AAGACATTGG | AGGTGTGTCC |
| | 3680 3710 TICTOTOGIO TOACHTAIT GOACAACTA CCTACAGAGA ITTAAA AAGACACCAC ACTOTATAA CCTGTTTOAT GOATGICICT AAAITI | TICTOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | TICKGGGTG AAGACACACTA AAGACACCAC AAGACAACTA AAGACACACTA AAGACACTACTA ATACACATTA ATACACATTA ATACACATTA ATACACACT AAATTTI ATACACACCT AAATTTI ATACACATTA ATACACATTA AATACACATTA AATACACACCT AAATTTI AAAAAATTTI AAAAATTTI AAAAAATTTI AAAAAATTTI AAAAAAAA | TICHGROAD 3690 3700 3710 3710 3710 3710 3710 3740 3750 3750 3760 3770 3770 3770 3770 3770 3770 377 | TICHGRGGIG ACTGIAITAN ANGACACCAC ACTGIAITAN ATACACATATT ATACACACCT ATACACACAT ATACACACATT ATACACACATT ATACACACATT ATACACACATT ATACACACATT ATACACACATT ATACACACATT ATACACACATT ATACACACAC | TTCTGTGGTG ACTGTATTA CCTGTFTGAT GGALGAGA TTTAAAG AAGACACCAC ACTGTATAA CCTGTFTTGAT GGALGACTCT AAATTTC AATAAATTTT AATTTTAAAA ATTCACATAT TACACAATTT GATGGTGGA ATTAAC AATAAATTTT AATTTTAAAA ATTCACATAT TACACAATTT GATGGTGGA ATTAAC AATAAATTTT AATTTTAAAA ATTCACATAT TACACAATTT GATGGTGGA ATTAAC AATTCCAACCT ATGGAACTGA TGAATGGGAG CAGTGGTGGA ATTAAC AATTCCAACCT ATGGAACTGA TGAATGGGAG GTCACTGACT ACTTACCCTC GTCACCACCT TACGGAA AATTCCAACCT ACTTACCCTC GTCACTACTC AATTAAGGTTGGA AATTCCAACCT ACTTACCCTC GTCACCACCT TACGGAA AACTAAGATTTTT AAGGTTGATAAAAA GAGACTC AAAAAAAAAA GAGACTA AAAAATTTC AATTCCAACCT TACACAAAAAAA GAGACTA AAAAAAAAAA | TICTOTGGTA AGGACACCAC ACTOINITHA CCTCTTTGAT AGGACACCAC ACTOINITHA CCTCTTTGAT ATAMATITT ATAMATITT ATAMATITT ATAMATITT ATAMATITT ATACTORAC ATGAAACTGA ATGAAACTGA TACACAATTT ATTCCAACCT TACACAATTT ATCCCAACCT TACACAATTT ATCCCAACCT TACACAATTT TACACAATTT TACACAATTT ATTCCAACCT TACACAATTT ACCATTTTACATT TACACATTTTACATT TACACATTTTACATT TACACATTTTACATT TACACATTTACATT TACACATTTACATTTACATT TACACATTTACATTTACATTTACATTTACATTACATTTACATTTACATTACACATTACACATTACACATTACACATTACACATTACACATTACACACATTAC | TICTOTOGGTO 3590 3710 3710 3710 3710 3710 3710 3710 371 |

38/53

FIG. 19H Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

| 2 | 4260 TGACTAGAGA ACTGATCTCT | 4320 CTCCCACACC GAGGGTGTGG | 4380 TTTATTGCAG AAATAACGTC | 4440 GCATTTTTT CGTAAAAAAA | 4500 GTCTGGATCG CAGACCTAGC | 4560 CCCAACTTGT GGGTTGAACA | 4620 ACAATAAAG TGFFTATTTC | 4680 TCTTATCATG AGAATAGTAC | 4740 CTGTTTCCTG GACAAAGGAC | 4800 ATAAAGTGTA TATTTCACAT |
|---|--------------------------------------|--------------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|
| 2 | 4250 TATAGIGCCT ' | 4310 TITAAAAAAC AAATITITIG | 4370 TGTTAACTTG ACAATTGAAC | 4430 CACAAATAAA GTGTTATTT | 4490 ATCTTATCAT TAGAATAGTA | 4550 CTTCGCCCAC GAAGCGGGTG | 4610 CACAAATTC GTGTTTAAAG | 4670 CATCAATGTA GTAGTTACAT | 4730 ATGGTCATAG TACCAGTATC | 4790 AGCCGGAAGC TCGGCCTTCG |
| | 4240 ATATTTGATG | 4300 TTTTACTTGC | 4360 CAATTGTTGT GTTAACAACA | 4420 TCACAAATIT AGTGTITAAA | 4480 TCATCAATGT AGTAGTTACA | 4540 TGCTGGAGTT ACGACCTCAA | 4600 GCANTAGCAT CGTYATCGTA | 4660 TGTCCAAACT ACAGGTTTGA | 4720 TGGCGTAATC ACCGCATTAG | 4780 acaacatacg tgttgtatgc |
| | 4230 TTAATAAGGA 1 | 4290 TTTGTAGAGG | 4350 AAAATGAATG TTTTACTTAC | 4410 AGCAATAGCA TCGTTATCGT | 4470 TTGTCCAAAC AACAGGTTTG | 4530 GGGGATCTCA CCCCTAGAGT | 4590 TACAAATAAA ATGTTTATTT | 4650 AGTTGTGGTT TCAACACCAA | 4710 AGCTAGAGCT TCGATCTCGA | 4770 ACAATTCCAC TGTTAAGGTG |
| | 4220 rgraaagggg 1 acattrcccc 1 | 4280 CCATACCACA GGTATGGTGT | 4340 CCTGAAACAT GGACTTTGTA | 4400 TTACAAATAA AATGTTTATT | 4460 TAGTTGTGGT ATCAACACCA | 4520 CCTCCAGCGC GGAGGTCGCG | 4580 TTATATGGT AATATTACCA | 4640 ACTGCATTCT TGACGTAAGA | 4700 GTCGACCTCT CAGCTGGAGA | 4760 TTATCCGCTC AATAGGCGAG |
| | 4210 CTTTTTAATT 7 GAAAAATTAA | 4270 TCATAATCAG (AGTATTAGTC (| 4330 TCCCCTGAA AGGGGGACTT | 4390 CTTATAATGG GAATATTACC | 4450 CACTGCATTC GTGACGTAAG | 4510 GCTGGATGAT CGACCTACTA | 4570 TTATTGCAGC AATAACGTCG | 4630 CATTTTTC GTAAAAAAG | 4690 TCTGTATACC AGACATATGG | 4750 TGTGAAATTG ACACTTTAAC |
| | | | | | | | | | | |

FIG. 19I Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

| pD17-hG1b | 4860 TCACTGCCCG AGTGACGGGC | 4920 cacacaacak acacacccr | 4980 CTGCGCTCGG GACGCGAGCC | 5040 TTATCCACAG AATAGGTGTC | 5100 GCCAGGAACC CGGTCCTTGG | 5160 GAGCATCACA CTCGTAGTGT | 5220 TACCAGGCGT ATGGTCCGCA | 5280 ACCGGATACC TGGCCTATGG | 5340 TGTAGGTATC ACATCCATAG | 5400 CCCGTICAGC GGGCAAGTCG |
|-----------|----------------------------------|-------------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|-----------------------------------|----------------------------------|
| G | 4850 TGCGTTGCGC | 4910 AATCGGCCAA TTAGCCGGTT | 4970 CACTGACTCG GTGACTGAGG | 5030 GGTAATACGG CCATTATGCC | 5090 CCAGCAAAAG GGTCGTTTTC | 5150 CCCCCTGAC GGGGGGACTG | 5210 ACTATAAAGA TGATATITCT | 5270 CCTGCCGCTT GGACGGCGAA | 5330 ATGCTCACGC TACGAGTGCG | 5390 GCACGAACCC CGTGCTTGGG |
| | 4840 TCACATTAAT 7 | 4900 TGCATTAATG A | 4960 CTTCCTCGCT GAAGGAGCGA | 5020 ACTCAAAGGC TGAGTTTCCG | 5080 GAGCAAAAGG CTCGTTTTCC | 5140 ATAGGCTCCG TATCCGAGGC | 5200 ACCCGACAGG TGGGCTGTCC | 5260 CTGTTCCGAC GACAAGGCTG | 5320 CGCTTTCTCA GCGAAAGAGT | 5380 TGGGCTGTGT ACCCGACACA |
| | 4830 GTGAGCTAAC CACTCGATTG | 4890 TCGTGCCAGC 7 | 4950 CGCTCTTCCG GCGAGAAGGC | 5010 GTATCAGCTC CATAGTCGAG | 5070 AAGAACAIGI ITCIIGIACA | 5130 GCGTTTTTCC CGCAAAAAGG | 5190 AGGTGGCGAA TCCACCGCTT | 5250 Grecectete Caceceaga | 5310 GGAAGCGTGG CCTTCGCACC | 5370 CGCTCCAAGC GCGAGGTTCG |
| | 4820 TGCCTAATGA C | 4880 GGGAAACCTG | 4940 GCGTATTGGG CGCATAACCC | 5000 GCGGCGAGCG CGCCGCTCGC | 5060 TAACGCAGGA ATTGCGTCCT | 5120 CGCGTTGCTG GCGCAACGAC | 5180 CTCAAGTCAG GAGTTCAGTC | 5240 AAGCTCCCTC TTCGAGGGAG | 5300 TCTCCCTTCG AGAGGGAAAGC | 5360 GTAGGICGIT CAICCAGCAA |
| | 4810 AAGCCTGGGG T | 4870 CTITICCAGIC G GAAAGGICAG | 4930 GAGGCGGTTT CTCCGCCAAA | 4990 TCGTTCGGCT AGCAAGCCGA | 5050 AATCAGGGGA TYAGTCCCCT | 5110 GTAAAAAGGC CATTYTYCG | 5170 AAAATCGACG TTTTAGCTGC | 5230 TICCCCCTGG AAGGGGGACC | 5290 TGTCCGCCTT ACAGGCGGAA | 5350 TCAGTTCGGT AGTCAAGCCA |
| | | | | | | | | | | |

FIG. 19J Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

| G15H-710d | 5460 | 5520 | 5580 | 5640 | 5700 | 5760 | 5820 | 5880 | 5940 | 6000 |
|-----------|------------|------------|------------|------------|------------|------------|------------|-------------|------------|------------|
| | AGACACGACT | GIAGGCGGIG | GTATITGGTA | TGATCCGGCA | ACGCGCAGAA | CAGTGGAACG | ACCTAGATCC | ACTIGGICIG | TITCGIICAI | TTACCATCTG |
| | TCTGTGCTGA | CATCCGCCAC | CATAAACCAT | ACTAGGCCGT | TGCGCGTCTT | GTCACCTTGC | TGGATCTAGG | TGAACCAGAC | AAAGCAAGIA | AATGGTAGAC |
| 2 | 5450 | 5510 | 5570 | 5630 | 5690 | 5750 | 5810 | 5870 | 5930 | 5990 |
| | CAACCCGGTA | AGCGAGGIAT | TAGAAGGACA | TGGTAGCTCT | GCAGCAGAIT | GTCTGACGCT | AAGGATCTIC | ATATGAGTAA | GATCTGTCTA | ACGGGAGGGC |
| | GTTGGGCCAT | TCGCTCCATA | ATCTTCCTGT | ACCATCGAGA | CGTCGTCIAA | CAGACTGCGA | TTCCTAGAAG | TATACTCATT | CTAGACAGAT | TGCCCTCCCG |
| | 5440 | 5500 | 5560 | 5620 | 5680 | 5740 | 5800 | 5860 | 5920 | 5980 |
| | GTCTTGAGTC | GGATTAGCAG | ACGGCTACAC | Gaaaaagagt | TTGTTTGCAA | TTTCTACGGG | GATTATCAAA | TCTAAAGTAT | CTATCTCAGC | TAACTACGAT |
| | CAGAACTCAG | CCTAATCGTC | TGCCGATGTG | Cttttccca | AACAAACGTT | AAAGATGCCC | CTAATAGITT | AGATTTCATA | GATAGAGTCG | ATTGATGCTA |
| | 5430 | 5490 | 5550 | 5610 | 5670 | 5730 | 5790 | 5850 | 5910 | 5970 |
| | GGTAACTATC | ACTGGTAACA | TGGCCTAACT | GTTACCTTCG | GGTGGTTTTT | CCTTTGATCT | TTGGTCATGA | TITAANICAA | AGTGAGGCAC | GTCGTGTAGA |
| | CCATTGATAG | TGACCATTGT | ACCGGATTGA | CAATGGAAGC | CCACCAAAAA | GGAAACTAGA | AACCAGTACT | AAAITIAGII | TCACTCCGTG | CAGCACATCT |
| | 5420 | 5480 | 5540 | 5600 | 5660 | 5720 | 5780 | 5840 | 5900 | 5960 |
| | CGCCTTATCC | GGCAGCAGCC | CTTGAAGTGG | GCTGAAGCCA | CGCTGGTAGC | TCAAGAAGAT | TTAAGGGATT | AAAATGAAGT | ATGCTTAATC | CTGACTCCCC |
| | GCGGAATAGG | CCGTCGTCGG | GAACTTCACC | CGACTICGGI | GCGACCATCG | AGTTCTTCTA | AATTCCCTAA | TTTTACTTCA | TACGAATTAG | GACTGAGGGG |
| | 5410 | 5470 | 5530 | 5590 | 5650 | 5710 | 5770 | 5830 | 5890 | 5950 |
| | CCGACCGCTG | TATCGCCACT | CTACAGAGIT | TCTGCGCTCT | AACAAACCAC | AAAAAGGAIC | AAACTCACG | TITTAAATTTA | ACAGITACCA | CCATAGTIGC |
| | GGCTGGCGAC | ATAGCGGTGA | GATGICICAA | AGACGCGAGA | TTGTTTGGTG | TTTTTCCTAG | TTTTQAGTGC | AAATTTAAA | TGICAAIGGI | GGTATCAACG |
| | | | | | | | | | | |

41/53

FIG. 19K Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

| מופע-/ומל | 6060 | 6120 | 6180 | 6240 | 6300 | 6360 | 6420 | 6480 | 6540 | 6600 |
|-----------|---------------------------------|---------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|
| | TTATCAGCAA | TCCGCCTCCA | AATAGTTTGC | GGTATGGCTT | TIGIGCAARA | GCAGIGITAI | GTAAGATGCT | CGGCGACCGA | ACTITABARG | CCGCTGTTGA |
| | AATAGTCGTT | AGGCGGAGGT | TTATCAAACG | CCATACCGAA | AACACGITIT | CGICACAAIA | CATTCTACGA | GCCGCTGGCT | TGAAATTITC | F GGCGACAACT |
| <u>a</u> | 6050 | 6110 | 6170 | 6230 | 6290 | 6350 | 6410 | 6470 | 6530 | 6590 |
| | GGCTCCAGAT | TGCAACTTTA | TTCGCCAGTT | CTCGTCGTTT | ATCCCCCATG | TAAGTIGGCC | CATGCCATCC | ATAGTGTATG | ACATAGCAGA | Arggatetta |
| | CCGAGGTCTA | ACGTTGAAAT | AAGCGGTCAA | GAGCAGCAAA | TAGGGGGTAC | AITCAACGGG | GTACGGTAGG | TATCACATAC | TGTATCGTCT | Ticctagaat |
| | 6040 | 6100 | 6160 | 6220 | 6280 | 6340 | 6400 | 6460 | 6520 | 6580 |
| | CACGCTCACC | GAAGTGGTCC | GAGTAAGTAG | TGGTGTCACG | GAGITACAIG | TTGTCAGAAG | CTCTTACTGT | CATTCTGAGA | ATACCGCGCC | Gararcictc |
| | GTGCGAGTGG | CTTCACCAGG | CTCATTCATC | ACCACAGTGC | CICAAIGIAC | AACAGTCTTC | GAGAATGACA | GTAAGACTCT | TATGGCGCGG | Cittigagag |
| | 6030 ccacdadacc caccreres | 6090 accabacaca cectcecet | 6150 CGGGAAGCIA GCCCTTCGAT | 6210 ACAGGCATCG TGTCCGTAGC | 6270 CGATCAAGGC GCTAGTTCCG | 6330 CCTCCGATCG GGAGGCTAGC | 6390 CIGCATAAIT GACGIAITAA | 6450 TCAACCAAGT AGTTGGTTCA | 6510 ATACGGGATA TATGCCCTAT | 6570 TCTTCGGGGGC |
| | 6020 TGCAATGATA (ACGITACTAT | 6080 AGCCGGAAGG | 6140 TAATTGTTGC ATTAACAACG | 6200 TGCCATTGCT ACGGTAACGA | 6260 CGGTTCCCAA GCCAAGGGTT | 6320 CTCCTTCGGT GAGGAAGCCA | 6380 TATGGCAGCA ATACCGTCGT | 6440 TGGTGAGTAC ACCACTCATG | 6500 CCCGGCGTCA GGGCCGCAGT | 6560 TGGAAAACGT ACCTTTTGCA |
| | 6010 | 6070 | 6130 | 6190 | 6250 | 6310 | 6370 | 6430 | 6490 | 6550 |
| | GCCCCAGIGC 7 | TABACCAGCC | TCCAGTCTAT | GCAACGITGT | CALTCAGCIC | AAGCGGITAG | CACTCATGGT | TTTCTGTGAC | GITGCICITG | TGCTCATCAT |
| | CGGGGTCACG 2 | ATTTGGTCGG | AGGTCAGATA | CGTTGCAACA | GTAAGICGAG | TTCGCCAATC | GTGAGTACCA | AAAGACACTG | CAACGAGAAC | ACCAGIAGIA |
| | | | | | | | | | | |

FIG. 19L
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

| 6660 TTIACITICA AAATGAAAGT | 6720 GGRATAAGGG CCFTATTCCC | 6780 AGCATTTATC TCGTAAATAG | 6840 AAACAAATAG TITGIITAIC | 6900 GGAGATCTGC CCTCTAGACG | 6960 TTARTITIAT AATTARAATA | 7020 GGTCGACTCT CCAGCTGAGA | 7080 CITOTGIGI GAACACAA | 7140 GCTTGACCGA CGAACTGGCT | 7200 NTGTACGGGC TACATGCCCG |
|--------------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|
| 6650 TTCAGCATCT ? | 6710 CGCAAAAAG GCGITITITC | 6770 ATATTATA TATAATAACT | 6830 TTAGAAAAT AATCITTIA | 6890 CGACGGATCG GCTGCCTAGC | 6950 ACCITITITI TGGAAAAAA | 7010 GATCCCCTAT CTAGGGGATA | 7070 CTGCTCCCTG GACGAGGGAC | 7130 ACAAGGCAAG TGTTCCGTTC | 7190 CTGCTTCGCG GACGAAGCGC |
| 6640 CCAACTGATC 1 GGITGACTAG 2 | 6700 GGCAAAATGC CCGITTTACG | 6760 TCCTTTTTCA AGGAAAAGT | 6820 TTGAATGTAT AACTTACATA | 6880 CACCTGACGI GTGGACTGCA | 6940 AGCCAGAGIA TCGGICICAI | 7000 CCGATCTCCC GGCTAGAGGG | 7060 Angccagtat TTCGGTCATA | 7120 TTAAGCTACA ANTICGAIGT | 7180 GCGTTTTGCG CGCAAAACGC |
| 6630 ACTCGTGCAC C TGAGCACGTG G | 6690 AAAACAGGAA C | 6750 CTCATACTCT GAGTATGAGA | 6810 GGATACATAT CCTATGTATA | 6870 CGAAAAGTGC GCTTTTCACG | 6930 GGCTTCGAAT CCGAAGCTTA | 6990 QAGITIGGCG CICAAACCGC | 7050 CCGCATAGTT GGCGTATCAA | 7110 CGAGCAAAAT GCTCGTTTTA | 7170 TTAGGGTTAG AATCCCAATC |
| 6620 GATGIAACCC P CIACAITGGG 1 | 6680 TGGGTGAGCA 1 | 6740 ATGITGAAIA IACAACITAI | 6800 TCTCATGAGC AGAGTACTCG | 6860 CACATITCCC GIGTAAAGGG | 6920 CHGGCGCGCC CTCCGCGCGG | 6980 TTTTGAGATG AAAACTCTAC | 7040 TGCTCTGATG ACGAGACTAC | 7100 GAGIAGIGEG CICAICACGE | 7160 AAGAATCTGC TTCTTAGACG |
| 6610 GAICCAGIIC G CIAGGICAAG | 6670 CCAGGGTTTC GGTCGCAAAG | 6730 CGACACGGAA GCTGTGCCTT | 6790 AGGGTTATTG TCCCAATAAC | 6850 GGGTTCCGCG CCCAAGGCGC | 6910 TAGGTGACCT ATCCACTGGA | 6970 TYTATTTAT AAATAAATA | 7030 CAGTACAATC GTCATGTTAG | 7090 GGAGGTCGCT CCTCCAGCGA | 7150 CANTTGCATG GITAACGTAC |

43/53

FIG. 19M Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

| pD17-hG1b | TIACGGGGTC AATGCCCCAG | 7320 ATGGCCCGCC TACCGGGCGG | 7380 TTCCCATAGT AAGGGTATCA | 7440 AAACTGCCCA TTTGACGGGT | 7500 TCAATGACGG AGTTACTGCC | 7560 CTACTTGGCA GATGAACCGT | 7620 AGTACATCAA TCATGTAGTT | 7680 TTGACGTCAA AACTGCAGIT | 7740 ACAACTCCGC TOTTGAGGCG | 7800 GCAGAGCICT CGICTCGAGA |
|-----------|--------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|----------------------------------|
| pD1; | 7250 | 7310 | 7370 | 7430 | 7490 | 7550 | 7610 | 7670 | 7730 | 7790 |
| | TAGTAATCAA | CITACGGIAA | ATGACGIAIG | TAITTACGGI | CCTATTGACG | TGGGACTITC | CGGITTIGGC | CTCCACCCA | AAATGICGIA | GICIATATAA |
| | ATCATTAGTT | GAATGCCAIT | TACTGCAIAC | ATANATGCCA | GGATAACTGC | ACCCTGAAAG | GCCAAAACCG | GAGGTGGGGT | TITACAGCAT | CAGATATAT |
| • | 7240 | 7300 | 7360 | 7420 | 7480 | 7540 | 7600 | 7660 | 7720 | 7780 |
| | TRGTTATTAA | CGTTACATAA | GACGICAAIA | ATGGGTGGAC | AAGTACGCCC | CATGACCITA | CATGGTGATG | ATTTCCAAGT | GGACTTFCCA | ACGGTGGGAG |
| | ATCAATAATT | GCAATGTATT | CIGCAGITAI | TACCCACCTG | TTCATGCGGG | GIACTGGAAI | GTACCACTAC | TAAAGGTTCA | CCTGAAAGGT | TGCCACCCTC |
| | 7230 | 7290 | 7350 | 7410 | 7470 | 7530 | 7590 | 7650 | 7710 | 7770 |
| | Gattattgac | TGGAGTTCCG | CCCGCCCATT | ATTGACGTCA | ATCATATGCC | ATGCCCAGTA | TCGCTATTAC | ACTCACGGGG | AAATCAACG | GIAGGCGIGI |
| | Ctaataactg | ACCTCAAGGC | GGGCGGGTAA | TAACTGCAGT | TAGTATACGG | TACGGGTCAT | AGCGATAATG | TGAGTGCCCC | TITTAGITGC | CATCCGCACA |
| | 7220 | 7280 | 7340 | 7400 | 7460 | 7520 | 7580 | 7640 | 7700 | 7760 |
| | CGITGACAIT | AGCCCATATA | CCCAACGACC | GGGACITICC | CATCAAGIGT | GCCTGGCALT | GIAITAGICA | TAGCGGTTTG | TITTGGCACC | CARATGGGCG |
| | GCAACIGIAA | TCGGGTATAT | GGGTTGCTGG | CCCTGAAAGG | GTAGITCACA | CGGACCGIAA | CATAAICAGI | ATCGCCAAAC | AAAACCGTGG | GTTTACCCGC |
| | 7210 | 7270 | 7330 | 7390 | 7450 | 7510 | 7570 | 7630 | 7690 | 7750 |
| | CAGATATACG | ATTAGITCAT | TGGCTGACCG | AACGCCAATA | CITGGCAGTA | TARATGGGCC | GIACATCTAC | TGGGCGTGGA | TGGGAGTTTG | CCCATTGACG |
| | GTCTATATGC | TAATCAAGIA | ACCGACTGGC | TTGCGGTTAT | GAACCGTCAT | ATTTACCGGG | CATGIAGATG | ACCCGCACCT | ACCCTCAAAC | GGGTAACTGC |

FIG. 19N
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

pD17-hG1b

CTGGCTAACT AGAGAACCCA CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG GACCGATTGA TCTCTTGGGT GACGAATGAC CGAATAGCTT TAATTATGCT GAGTGATATC

7870 GGAGACCCAA GCTT CCTCTGGGTT CGAA

7880

į

ŧ

FIG. 20
COMPLEMENT DEPENDENT CYTOTOXICITY

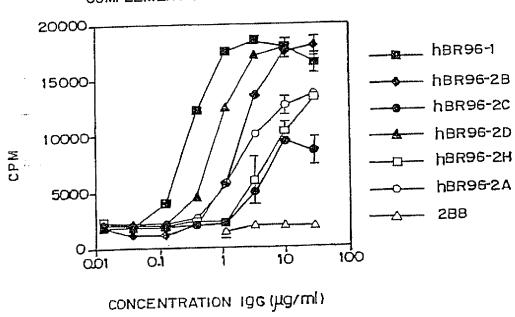
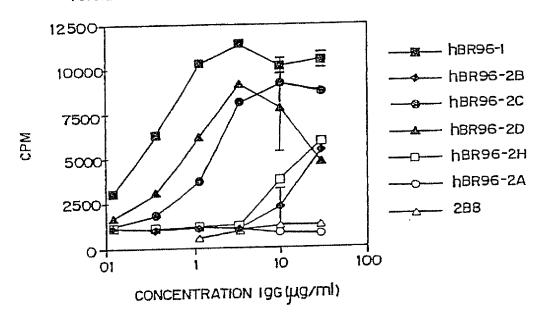


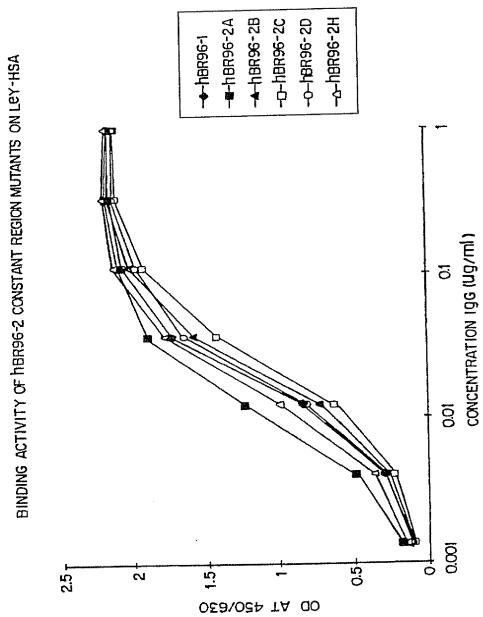
FIG. 21

ANTIBODY DEPENDENT CELL-MEDIATED CYTOTOXICITY



47/53

FIG.22



48/53 FIG.23

BINDING ACTIVITY OF HBR96-2 CONSTANT REGION MUTANTS ON LNFPIII-BSA

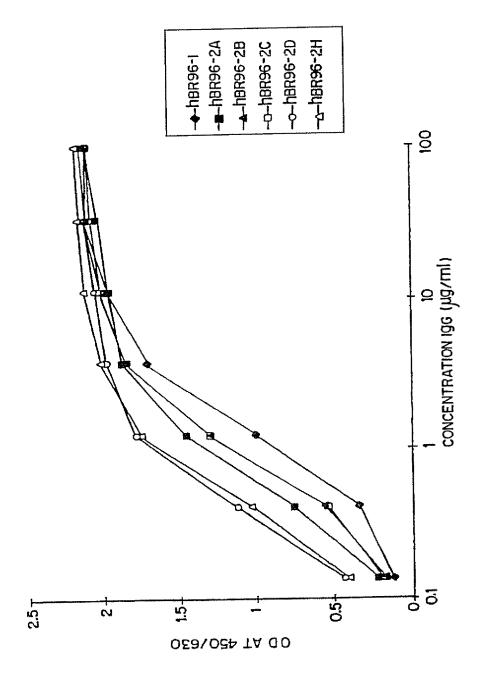


FIG. 24A

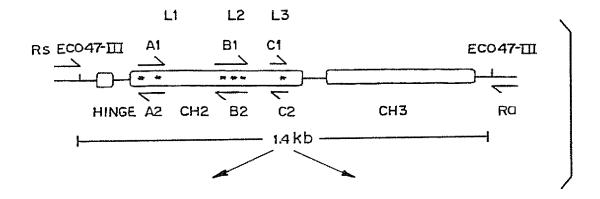
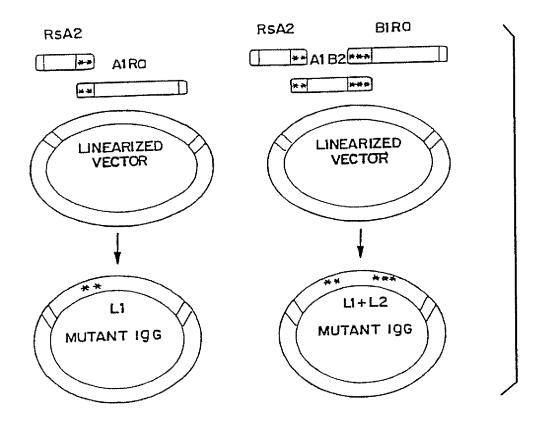


FIG. 24B



50/53 FIG.25

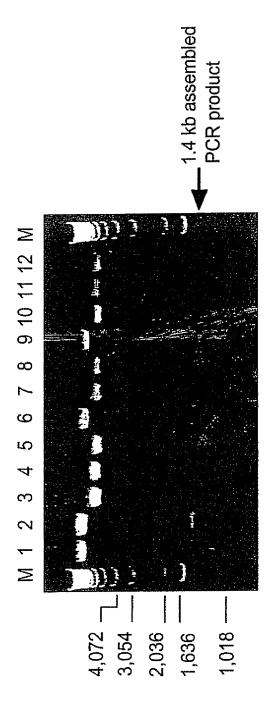


FIG. 26

hBR96-2 Heavy Chain Variable Region (VH)

(SEQ ID NO:24)

1 11 21 31 41
EVQLVESGGG LVQPGGSLRL SCAASGFPFS DYYMYWVRQA PGKGLEWVSY
51 61 71 81 91
ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL
101 111
ADGAWFAYWG QGTLVTVSS

Human IgGl Constant

(SEQ ID NO:25)

CH1.

A STKGPSVFPL APSSKSTSGG TAALGCLVKD

YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY
CH2 235 237
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CHAPELLGGP SVFLFPPKPK

·

DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS
318 320 322 331 CH3

TYRVVSVLTV LHQDWLNGKÈ YKDKVSNKAL PAPIEKTISK AKGQPREPQV

YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL

DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK

FIG. 27

hBR96-2A: Heavy Chain Variable Region (V_H)

(SEQ ID NO:24)

1 11 21 31 41
EVQLVESGGG LVQPGGSLRL SCAASGFPFS DYYMYWVRQA PGKGLEWVSY
51 61 71 81 91
ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL
101 111
ADGAWFAYWG QGTLVTVSS

hBR96-2A: Human Heavy Chain IgGl Constant Region △CH2

(SEQ ID NO:26)

A STRGPSVFPL APSSKSTSGG TAALGCLVKD YFPEFVTVSW NSGALTSGVH
TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK
SCDKTHTCPP CP GQPREPQV YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA
VEWESNGQPE NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM
HEALHNHYTQ KSLSLSPGK

FIG. 28

(SEQ ID NO:27)

This sequence is the chi BR96 IgGl with CH2 deleted.

VH

- 1 EVNLVESGGG LVQPGGSLKV SCVTSGFTFS DYYMYWVRQT PEKRLEWVAY
- 51 ISQGGDITDY PDTVKGRFTI SRDNAKNTLY LQMSRLKSED TAMYYCARGL CH1
- 101 DDGAWFAYWG QGTLVTVSVA STKGPSVFPL APSSKSTSGG TAALGCLVKD
- 151 YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY
- 201 ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPGQPREPQV YTLPPSRDEL
- 251 TKNOVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS
- 301 KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK